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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:43:01 ; Search time 26.57 Seconds
(without alignments)
178.884 Million cell updates/sec

Title: US-09-203-768a-2

Perfect score: 748
Sequence: 1 MKHMFELLVAAPRWVLSQ.....ARPHRYPDYWGQGLTVVSS 139

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_36:*

- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	622	83.2	116	16	Human immunoglobulin
2	588	78.6	139	21	Human PTHrP monocl
3	580	77.5	139	21	Human 5' EST relat
4	575.5	76.9	472	17	Anti-Thesius D reco
5	566	75.7	244	20	Amino acid sequenc
6	560.5	74.9	136	18	Immunoglobulin RB6
7	558.5	74.7	123	17	Anti-Thesius D mono
8	558.5	74.7	142	14	FI05 rearranged va
9	552	73.8	128	12	Anti-human RHD FOM
10	550	73.5	116	14	Vh 71-4. Homo sap
11	550	73.5	116	16	Human immunoglobul
12	543	72.6	141	21	Amino acid sequenc

13	541.5	72.4	476	18	W01822
14	541.5	72.4	476	19	W63765
15	539.5	72.1	470	21	Y44721
16	539	72.1	118	16	R66348
17	539	72.1	475	17	R93553
18	538	71.9	116	16	R66298
19	536.5	71.7	140	18	W32477
20	536.5	71.7	140	19	W43430
21	536.5	71.7	140	21	Y56732
22	536.5	71.7	141	14	R31948
23	536.5	71.7	467	18	W14927
24	536.5	71.7	467	18	W14925
25	536.5	71.7	467	18	W14926
26	536	71.7	139	21	Y56713
27	536	71.7	141	19	W70378
28	532.5	71.2	139	18	W35284
29	532.5	71.2	139	18	W14922
30	532.5	71.2	139	19	W53988
31	532.5	71.2	143	15	Y56706
32	530.5	70.9	134	15	R54049
33	530.5	70.9	134	17	W01526
34	530.5	70.9	134	18	W24986
35	530	70.9	140	21	Y64689
36	529.5	70.8	121	12	R12270
37	529.5	70.8	476	18	W01818
38	529.5	70.8	476	19	W63761
39	527	70.5	118	16	R66329
40	527	70.5	125	9	P81259
41	526.5	70.4	139	19	W57446
42	526.5	70.4	155	21	Y64727
43	521	69.7	118	16	R66342
44	517	69.1	205	20	Y34299
45	516.5	69.1	117	21	Y68899

ALIGNMENTS

RESULT 1	
ID R66324	R66324 standard; Protein: 116 AA.
XX AC R66324;	
XX DT 03-AUG-1995 (first entry)	
XX DE Human immunoglobulin variable heavy chain #30.	
XX KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;	
XX KW cosmid; placenta; vector; pUB81; E.coli; mammalian.	
XX OS Homo sapiens.	
XX PN W09426895-A.	
XX PD 24-NOV-1994.	
XX PF 10-MAY-1993; 93WO-JP00603.	
XX PR 10-MAY-1993; 93WO-JP00603.	
XX PA (NIBS) JAPAN TOBACCO INC.	
XX PI Honjo T, Matsuda F;	
XX DR WPI: 1995-006791/01.	
XX DR N-PSDB: Q78972.	
XX PT DNA fragment comprising human immunoglobulin Vh genes - for the	
XX PT production of human immunoglobulin in mammalian hosts	
XX PS Claim 41; Page 74-75; 130pp; Japanese.	

Primitised anti-hu
Macaque primate
Human immune syste
Human immunoglobul
Monoclonal antibod
Human immunoglobul
Anti-CD4 cynomolg
Monkey anti-CD4 he
Amino acid sequenc
Anti-CD4 Vh peptid
Human gamma-4PE he
Human gamma-4 heav
Human gamma-4E hea
Amino acid sequenc
Anti-human CD23 6G
Monkey anti-human
Monkey anti-CD4 he
Anti-CD4 antibody
Murine anti-erythr
Sequence of the Vh
Monoclonal antibod
Monoclonal antibod
Human 5' EST relat
Anti-human RHD FOM
Primate anti-hu
Macaque primate
Human immunoglobul
Human immunoglobul
Anti-CD4 antibody
Human 5' EST relat
Human immunoglobul
IgM antibody CEM 1
The variable regio

CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
 CC sequences encoded by novel isolated genes. The genes (Q78939-79002) were
 CC isolated and cloned from a series of cosmid constructs: Y102; Y103; Y21;
 CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers
 CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
 CC fragments cover a region of 800 kb. The DNA fragments were isolated from
 CC high molecular weight DNA from human placenta. The DNA was partially
 CC digested with TaqI restriction enzyme. The fragments were separated by
 CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
 CC were ligated with ClaI-digested cosmid vector pUB81. The ligation
 CC products were in vitro packed and infected into E.coli 490A. The
 CC fragments were then subcloned by colony hybridisation. The Vh genes and
 CC the DNA fragments encoding them are useful in producing human
 CC immunoglobulin in mammalian hosts.

CC Sequence 116 AA:

Query Match 83.2%; Score 622; DB 16; Length 116;
 Best Local Similarity 100.0%; Pred. No. 8.5e-45;
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKNLWFFLLVAAPRWVLSQVLOQWAGLKPSETLSLTCAVYGGSFSGYIWSWIRPP 60
 DB 1 MKNLWFFLLVAAPRWVLSQVLOQWAGLKPSETLSLTCAVYGGSFSGYIWSWIRPP 60
 OY 61 GKGLEWIGELINSGSTNYPNLSKSRVTISVDTSKNQFSLKLSVTADPAAVYCAEIAA 120
 DB 61 GKGLEWIGELINSGSTNYPNLSKSRVTISVDTSKNQFSLKLSVTADPAAVYCAEIAA 120

RESULT 2
 Y82628
 ID Y82628 standard; Protein: 139 AA.

AC Y82628;
 DT 02-AUG-2000 (first entry)

DE Human PTHrP monoclonal antibody clone 4B4-6-21 protein SEQ ID NO:40.

KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingivitis;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cycostatic; antiinflammatory.

OS Homo sapiens.

Key Location/Qualifiers
 FH Misc-difference 77
 FT /note="possibly Tyr"

PN JP2000080100-A.

PD 21-MAR-2000.

PE 12-OCT-1998; 98JP-0304793.

PR 17-JUN-1998; 98JP-0188196.

PR 26-JUN-1998; 98JP-0196729.

PA (NIBS) JAPAN TOBACCO INC.

DR WPI: 2000-286723/25.

DR N-PSDB; A13938.

PT A human monoclonal antibody to parathyroid hormone related protein.
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 PS Claim 32; Page 75; 88pp; Japanese.

CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cycostatic and
 CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone protein sequence from the
 CC present invention.

CC Sequence 139 AA:

Query Match 78.6%; Score 588; DB 21; Length 139;
 Best Local Similarity 82.0%; Pred. No. 6.5e-42;
 Matches 114; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

OY 1 MKNLWFFLLVAAPRWVLSQVLOQWAGLKPSETLSLTCAVYGGSFSGYIWSWIRPP 60
 DB 1 MKNLWFFLLVAAPRWVLSQVLOQWAGLKPSETLSLTCAVYGGSFSGYIWSWIRPP 60
 OY 61 GKGLEWIGELINSGSTNYPNLSKSRVTISVDTSKNQFSLKLSVTADPAAVYCAEIAA 120
 DB 61 GKGLEWIGELINSGSTNYPNLSKSRVTISVDTSKNQFSLKLSVTADPAAVYCAEIAA 120
 OY 121 RPHRYFDYWGCGTLTVVSS 139
 DB 121 YYYGIDVWGGTTLTVVSS 139

RESULT 3
 Y64676
 ID Y64676 standard; Protein: 139 AA.

AC Y64676;

DT 01-FEB-2000 (first entry)

DE Human 5' EST related polypeptide SEQ ID NO:837.

KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
 KW gene therapy; chromosome mapping; upstream regulatory sequence;
 KW forensic; location; development; protein synthesis; stability;
 KW regulation; identification.

OS Homo sapiens.

PN W09953051-A2.

PD 21-OCT-1999.

PE 09-APR-1999; 99WO-1B00712.

PR 09-APR-1998; 98US-0057719.

PR 28-APR-1996; 98US-0069047.

PA (GENET) GENSET.

PI Dumas Mline Edwards J, Duclert A, Giordano J;

DR WPI: 2000-038446/03.

DR N-PSDB; Z42290.

PT Novel secreted protein 5' expressed sequence tag sequences used in
 PT diagnostic, forensic, gene therapy, and chromosome mapping procedures
 PS Claim 3; Page 605-606; 837pp; English.
 PS Z42265 to Z43075 represent novel 5' expressed sequence tag (EST)

FT	Region	/note= "complementarity determining region"
FT		98.112
FT		/label= CDR3
FT		/note= "complementarity determining region"
PN	FR2724182-A1.	
PD	08-MAR-1996.	
XX		
PF	02-SEP-1994;	94FR-0010566.
XX		
PR	02-SEP-1994;	94FR-0010566.
XX		
PA	(INSP) INST PASTEUR.	
PA	(PROT -) PROTEINE PERFORMANCE.	
XX		
PI	Chaabih H, Edelman L, Kaczorek M, Margaritte C;	
XX		
DR	WPI; 1996-162018/17.	
DR	N-PSDB; T26870.	
XX		
PT	Recombinant anti-rhesus D monoclonal antibody - expressed by	
PT	Baculovirus-transformed insect cells and useful for preventing	
PT	haemolysis in new-born babies	
XX		
PS	Example 1: Page 32; 46pp; French.	
XX		
CC	The human monoclonal antibody D7C2, of isotype IgM, recognises a	
CC	30-32 kD polypeptide on the membrane of rhesus positive red blood	
CC	cells. The antibody agglutinates rhesus positive cells but not	
CC	rhesus negative cells and is useful diagnostically and also for	
CC	preventing haemolysis in new-born rhesus positive babies.	
CC	Recombinant IgM-D7C2 can be produced by insect cells which have	
CC	been transformed by a baculoviral vector comprising a D7C2	
CC	expression cassette. The present sequence is that of the variable	
CC	region of the IgM-D7C2 heavy chain.	
XX		
SO	Sequence 123 AA;	

Query Match	74.7%	Score 558.5	DB 17	Length 123
Best Local Similarity	86.6%	Pred No. 1.6e-39		
Matches 109	Conservative 3	Mismatches 8	Indels 3	Gaps 2

QY	20	OVOLOOMAGAGLLKPSSETLSLTCAYVGGSEFGYWSNIRPPGKGLWIGELINHSGSTNN	79
Db	1	qyqlqwgagallkpsetlsltctcyggsfsgywwslrqpqpgkglewigeinhsgstnn	60
QY	80	PSLKRRLVITSVDTSKNOSIKLSYTAAPFAYYCAR--EINARPH-RXEDYWGCGTLVT	136
Db	61	PSLKRRLVITSVDTSKNOSIKLSYTAAPFAYYCARPEYKWKYHGDFDPWGGQTLVT	120
QY	137	VSS	139
Db	121	VSS	123

RESULT	8
R41285	
ID	R41285 standard; Protein: 142 AA.
XX	
AC	R41285;
XX	
DT	01-NOV-1993 (first entry)
XX	
DE	F105 rearranged variable region heavy chain.
XX	
KM	Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
KW	CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
XX	chain; epitope; immune deficiency.
OS	Homo sapiens.

XX	Key	location/Qualifiers
XX	Peptide	1..19
XX	Protein	/label= sig_peptide
XX		20..142
XX		/label= mat_protein
XX	W09312232-A.	
XX	24-JUN-1993.	
XX	10-DEC-1992;	92WO-US10928.
XX	10-DEC-1991;	91US-0804652.
XX	(DAND) DANA FARBER CANCER INST INC.	
XX	(NEME-) NEW ENGLAND DEACONNESS HOSPITAL CORP.	
XX	Haseltine WA, Marasco WA, Posner MK, Sodroski JG;	
XX	WPI; 1993-214174/26.	
XX	N-PSDB; Q49154.	
XX	DNA segments encoding monoclonal antibody - which binds to gp120	
XX	and neutralises HIV, for treating AIDS, and for diagnosing and	
XX	monitoring HIV infection	
XX	Claim 9-10; Page 77; 109pp; English.	
XX	mRNA from the known hybridoma F105 was converted to cDNA and this	
XX	subjected to PCR amplification using primers corresp. to appropriate	
XX	parts of the heavy or light chains and having restriction sites to	
XX	permit cloning. The extension prods. were isolated and sequenced.	
XX	The recombinant human monoclonal antibody (MAb) binds to a	
XX	discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks	
XX	the binding of gp120 to the CD4 receptor, and neutralises a broad	
XX	range of HIV isolates. The MAb may be used to treat immune	
XX	deficiency, esp. at doses of 0.1-10 mg/kg.	
XX	Sequence 142 AA;	

Query Match	74.7%;	Score 558.5;	DB 14;	Length 142;
Best Local Similarity	77.6%;	Pred. No. 1,8e-39;		
Matches 111;	Conservative 10;	Mismatches 17;	Indels 5;	Gaps 2.
OY	1	MKHLNFWLLVAAPRWVLSQVQLDQMGAGLLKPSFTSLTCAVYGGSFSGYTWMIROPP	60	
Db	1	mehlwfflllvaaprwvlsqvqlgespgvlvxpsetslstlcetvsgsgslshywsvlrqp	60	
OY	61	GKGLWEIGELINHGSGTNNPNSLKSQVTSVDPSKNOFSILKSSVVAADPAVYVCAREINA	120	
Db	61	gkglwvlgyllyysgstnpspslksrvtlstvelsknqfslklsmtdadavyygcargpvp	120	
OY	121	RPNRIFDY----WGQGLVTVSS	139	
Db	121	avf-ygdvrlpdpwggclvtvss	142	
RESULT	9			
R12269				
ID	R12269	standard; Protein; 128 AA.		
XX	AC	R12269;		
XX	DT	15-AUG-1991 (first entry)		
XX	DE	Anti-human Rhd FOM-1 Mab (VH chain).		
XX	KW	Monoclonal antibody; rhesus D; blood-typing; CDR;		
XX	OS	haemolytic disease of the newborn; HDN.		
XX		Homo sapiens.		

FH Key Location/Qualifiers
 FT Region 31..35 /label= CDR1
 FT Region 50..65 /label= CDR2
 FT Region 98..117 /label= CDR3
 FT Region /label= CDR3
 PN WO9107492-A.
 XX 30-MAY-1991.
 PD 30-MAY-1991.
 XX 13-NOV-1990; 90MO-EP01964.
 XX 13-NOV-1989; 89GB-0025590.
 XX (BLOO-) CENT BLOOD LAB AUTH.
 PA Hughes - Jones N;
 PI WPI: 1991-178104/24.
 DR N-PSDB; Q11951.
 XX
 PT DNA encoding complementary determining regions - of human
 PT anti-rhesus D antibodies, useful in prodn. of monoclonal
 PT antibodies and for passive immunisation
 PS Disclosure: Fig 8; 32pp; English.
 XX
 CC The DNA sequence of eleven monoclonal antibodies are
 CC represented in Q119145-57. Synthetic genes, for both heavy and
 CC light chains may be created by combining selected CDR 1, 2, and 3
 CC regions, which may be selected from different antibody mols. having
 CC varied binding specificity. The chimeric anti-Rhd antibodies can be
 CC used for diagnosis and therapy, and are capable of providing blood-
 CC typing reagents of high specificity and reliability. They can also
 CC be used in passive immunisation to prevent haemolytic disease of the
 CC newborn.
 CC
 XX
 SQ Sequence 128 AA;

Query Match 73.8%; Score 552; DB 12; Length 128;
 Best Local Similarity 83.7%; Pred. No. 5.7e-39;
 Matches 108; Conservative 4; Mismatches 7; Indels 10; Gaps 2;

QY 20 QYOLQOMGAGLKPSETLSLTCAYVGGSGFYWSWIRPPKGLGELINHSSTNN 79
 DB 1 qvqlqwgagllkpselstlcaavgssitsgywmwlrppqkglewlgelhsstnyn 60
 QY 80 PSLKSRVTISVDTSKNQFSLKSSVTAADTAVYYCCARETIAARPHR-----YFDYWG 130
 DB 61 pslkervtmsvtsknqfslkssvtaadtaavycargl-erplnqllnrlgyymdwvg 119
 QY 131 OGTEVTSS 139
 DB 120 kgtvtvss 128

RESULT 10
 R42689 R42689 standard; Protein; 116 AA.
 AC R42689;
 DT 01-NOV-1993 (first entry)
 DE Vh 71-4.
 XX Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
 KW CDR; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency.
 XX

OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19 /label= sig_peptide
 FT Protein 20..116 /label= mat_protein
 FT Region 49..54 /label= CDR1
 FT Region 69..84 /label= CDR2
 FT Region /label= CDR2
 PN WO9312232-A.
 XX 24-JUN-1993.
 PD 24-JUN-1993.
 XX 10-DEC-1992; 92WO-US10928.
 XX 10-DEC-1991; 91US-0804652.
 XX (DAND) DANA FARBER CANCER INST INC.
 PA (NEWME-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
 XX Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
 PI WPI: 1993-214174/26.
 DR N-PSDB; Q42697.
 XX
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Disclosure: Page 64; 109pp; English.
 XX
 CC The nucleotide sequence of rearranged F105 Vh (Q42698) was compared
 CC to two monoclonal antibodies (Ab26 - Q42702) and 268-D - Q42703),
 CC which by nucleotide sequence analysis, appear to use a rearranged
 CC Vh 71-4 gene (Q42697).
 CC Ab26 (Q42702) was derived from CD5+ B cells of a healthy donor and
 CC represents a naturally occurring polyclonal antibody which binds to
 CC many antigens. Ab26 shares greatest sequence similarity with germline
 CC Vh 71-4.
 CC
 XX
 SQ Sequence 116 AA;

Query Match 73.5%; Score 550; DB 14; Length 116;
 Best Local Similarity 90.5%; Pred. No. 7.5e-39;
 Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKHMFELLVAAPRWVLSOVOLQMGAGLKPSETLSLTCAYVGGSGFYWSWIRPP 60
 DB 1 mkhlwfflllvaaprwvlsqvqlqesgplvkrpselstlcvsgsvssywsywrpp 60
 QY 61 GKLEWIGELINHSSTNNPSLSKRVITISVDTSKNQFSLKSSVTAADTAVYYCAR 116
 DB 61 gkglewlgelinygstnpslskrtvtsvdtksknqfslkssvtaadtaavycar 116

RESULT 11
 R66346 R66346 standard; Protein; 116 AA.
 AC R66346;
 DT 04-AUG-1995 (first entry)
 DE Human immunoglobulin variable heavy chain #52.
 XX
 KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJBB1; E.coli; mammalian.
 XX Homo sapiens.
 OS


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XX XX WO9426895-A.
XX PN
XX XX 24-NOV-1994.
XX PD
XX XX
XX PF 10-MAY-1993; 93WO-JP00603.
XX XX
XX PR 10-MAY-1993; 93WO-JP00603.
XX XX
XX PA (NISB ) JAPAN TOBACCO INC.
XX XX
XX PI Honjo T, Matsuda F;
XX XX
XX DR WPI: 1995-006791/01.
XX DR N-PSDB: Q78997.
XX PT
XX PR DNA fragment comprising human immunoglobulin Vh genes - for the
XX PT production of human immunoglobulin in mammalian hosts
XX PS
XX XX Disclosure: Page 107-108; 130pp; Japanese.
XX CC
XX CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
XX CC sequences encoded by novel isolated genes. The genes (Q78939-78002) were
XX CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
XX CC Y6; Y24; 3-31; M84; M18 and M31, by PCR amplification using primers
XX CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
XX CC fragments cover a region of 800 kb. The DNA fragments were isolated from
XX CC high molecular weight DNA from human placenta. The DNA was partially
XX CC digested with TaqI restriction enzyme. The fragments were separated by
XX CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
XX CC were ligated with ClaI-digested cosmid vector pUB1. The ligation
XX CC products were in vitro packed and infected into E.coli 490A. The
XX CC fragments were then subcloned by colony hybridisation. The Vh genes and
XX CC the DNA fragments encoding them are useful in producing human
XX CC immunoglobulin in mammalian hosts.
XX XX
XX SQ Sequence 116 AA:

Query Match 73.5%; Score 550; DB 16; Length 116;
Best Local Similarity 90.5%; Pred. No. 7.5e-39;
Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 MKHLFFLLVAPRWVLSQVLOQMGAGILKRPSETLSTCAVYGSFSGYYMSWIROPP 60
DB 1 mkhlwfflllvaprwvlsqvgldesgpglvkpselstlctcvsgsvsywvtrpp 60
QY 61 GKGLEWIGEINHSGSTNPNPSLKSRVTSVDTSKNQFSKLSSVTAADTAVYYCAR 116
DB 61 gkglewiygyysgscnypslksrvtlsdvtsknqfslkssvtaadtavyycaar 116

RESULT 12
Y56728
ID Y56728 standard; protein; 141 AA.
XX
XX AC Y56728;
XX
XX DT 15-FEB-2000 (first entry)
XX
XX DE Amino acid sequence of Cynomolgus VH cDNA clone 2-5.
XX
XX KW Complementarity determining region; antibody; primate; immunogenicity;
XX KW Old World ape; Old World monkey; antigen-binding affinity.
XX
XX OS Macaca cynomolgus.
XX
XX PN WO9553369-A1.
XX
XX PD 04-NOV-1999.
XX
XX PF 28-APR-1999; 99WO-US09131.
XX

```

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PR 28-APR-1998; 98US-0083367.
XX
XX XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX XX
XX PI Taylor AH;
XX
XX DR WPI: 2000-023265/02.
XX DR N-PSDB: 239331.
XX
XX PT Antibodies containing donor complementarity determining regions and
XX PT non-human primate acceptor frameworks, having reduced immunogenicity in
XX PT humans -
XX
XX PS Example 3; Page 79; 123pp; English.
XX
XX CC The invention provides an antibody (Ab) comprising donor CDRs
XX CC (complementarity determining regions) derived from a non-human antigen-
XX CC specific donor antibody, and an acceptor framework from a non-human
XX CC primate. The Abs are prepared by grafting CDRs from a non-human antigen-
XX CC specific donor antibody onto homologous Old World ape or monkey acceptor
XX CC frameworks. The Abs have reduced immunogenicity and are better tolerated
XX CC in humans (because of the close similarity between the human and primate
XX CC proteins), but retain the full antigen-binding affinity of the donor
XX CC antibody.
XX
XX SQ Sequence 141 AA:

Query Match 72.6%; Score 543; DB 21; Length 141;
Best Local Similarity 75.2%; Pred. No. 3.5e-38;
Matches 106; Conservative 10; Mismatches 23; Indels 2; Gaps 2;

QY 1 MKHLFFLLVAPRWVLSQVLOQMGAGILKRPSETLSTCAVYGSFSGYYMSWIROPP 60
DB 1 mkhlwfflllvaprwvlsqvgldesgpglvkpselstlctcvsgsvfctyywnvtrpp 60
QY 61 GKGLEWIGEINHSGS-TNPNPSLKSRVTSVDTSKNQFSKLSSVTAADTAVYYCAR 119
DB 61 gkglewiygy199gggprpnyslksrvtlsdvtsknqfslkssvtaadtavyycaardtg 120
QY 120 -ARPHRFDPYWGCGTLVTVSS 139
DB 121 ygasndatfdwggjrvtvss 141

RESULT 13
W01822
ID W01822 standard; protein; 476 AA.
XX
XX AC W01822;
XX
XX DT 25-MAY-1997 (first entry)
XX
XX DE Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
XX
XX KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
XX KW primatised antibody; B7 antigen; CD28; immunosuppressive;
XX KW autoimmune disease; idiopathic thrombocytopenia purpura;
XX KW systemic lupus erythematosus; Rheumatoid arthritis; psoriasis;
XX KW type 1 diabetes mellitus; graft versus host disease;
XX KW hetero-hybridoma; transfectoma.
XX
XX OS Chimeric Macaca cynomolgus;
XX OS Chimeric Homo sapiens.
XX
XX PN WO9640878-A1.
XX
XX PD 19-DEC-1996.
XX
XX PF 06-JUN-1996; 96WO-US10053.
XX
XX PR 07-JUN-1995; 95US-0487550.
XX

```

PA (IDEC-) IDEC PHARM CORP.
 XX
 XX
 PI Anderson DR, Brams P, Hanna N, Shetlowsky WS;
 XX
 DR WPI: 1997-108638/10.
 DR N-PSDB: T62513.
 XX
 PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen
 XX useful for treating autoimmune disease or graft-versus-host disease
 PS Claim 14; Fig 10B; 81pp; English.
 XX
 XX 2 Polypeptides (W01821 and W01822) respectively comprise primatized
 CC forms of the light and heavy chains of cynomolgus monkey anti-human
 CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
 CC heavy variable genes (see also T62512 and T62513) are inserted into
 CC an expression vector (pref. NEOSPIRA) which contains human light and
 CC heavy chain constant region genes to allow prodn. of the primatized
 CC antibody in e.g. CHO cells. Primatized 7C10 and 7B6 anti-B7.1
 CC antibodies have also been produced (see also W01817-20). The
 CC primatized antibodies inhibit the B7/CD28 pathway, making them
 CC useful immunosuppressants for the treatment of autoimmune disorders
 CC and graft-versus-host disease.
 CC
 XX Sequence 476 AA;
 SQ
 Query Match 72.4%; Score 541.5; DB 18; Length 476;
 Best Local Similarity 74.0%; Pred. No. 1.6e-37;
 Matches 108; Conservative 11; Mismatches 20; Indels 7; Gaps 3;
 QY 1 MKHLMEFLLLVAPRWVLSQVLOQWAGLLKPSFTLSLTCAVYGSGFS-GYVMSWIRP 59
 DB 1 mkhlwfflllvaprwvlsqvldgespglvkpselstlcavsgsgisgrygwyirp 60
 QY 60 PKGLGEMIGET-NHSGSTINYPNLSKSRVTISVDTSKNPSLKLSVTADTAIVYICARE- 117
 DB 61 pKGLGEMIGET-NHSGSTINYPNLSKSRVTISVDTSKNPSLKLSVTADTAIVYICARE- 120
 QY 118 ----IAARHRYEDWGGSTLVTVSS 139
 DB 121 lfsvvgmylnwfdwpgvplvtvss 146
 RESULT 14
 W63765
 ID W63765 standard; Protein: 476 AA.
 AC W63765;
 XX
 DT 29-SEP-1998 (first entry)
 XX
 DE Macaque primatized 16C10 heavy chain protein.
 XX
 KW Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
 KW CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;
 KW T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;
 KW immunogen; anti-idiotypic reagent; interleukin-2; IgG; immunoglobulin G;
 KW T cell proliferation.
 OS Macaca fascicularis.
 XX
 PN W09819706-A1.
 PD 14-MAY-1998.
 XX
 XX 29-OCT-1997; 97WO-US19906.
 XX
 XX 08-NOV-1996; 96US-0746361.
 XX
 PA (IDEC-) IDEC PHARM CORP.
 XX
 PI Anderson DR, Brams P, Hanna N;

XX
 DR WPI: 1998-286601/25.
 DR N-PSDB: V35489.
 XX
 PT New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 XX inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 XX cells, e.g. graft rejection or tumours
 PS Example 7; Fig 5b; 87pp; English.
 XX
 XX This sequence represents a primatized form of the antibody 16C10 heavy
 CC chain from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma. Infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 CC
 XX Sequence 476 AA;
 SQ
 Query Match 72.4%; Score 541.5; DB 19; Length 476;
 Best Local Similarity 74.0%; Pred. No. 1.6e-37;
 Matches 108; Conservative 11; Mismatches 20; Indels 7; Gaps 3;
 QY 1 MKHLMEFLLLVAPRWVLSQVLOQWAGLLKPSFTLSLTCAVYGSGFS-GYVMSWIRP 59
 DB 1 mkhlwfflllvaprwvlsqvldgespglvkpselstlcavsgsgisgrygwyirp 60
 QY 60 PKGLGEMIGET-NHSGSTINYPNLSKSRVTISVDTSKNPSLKLSVTADTAIVYICARE- 117
 DB 61 pKGLGEMIGET-NHSGSTINYPNLSKSRVTISVDTSKNPSLKLSVTADTAIVYICARE- 120
 QY 118 ----IAARHRYEDWGGSTLVTVSS 139
 DB 121 lfsvvgmylnwfdwpgvplvtvss 146
 RESULT 15
 Y44721
 ID Y44721 standard; Protein: 470 AA.
 AC Y44721;
 XX
 DT 25-APR-2000 (first entry)
 XX
 DE Human immune system molecule, ISMO-2.
 XX
 KW Human; immune system molecule; ISMO-2; Incyte clone 2849752; diagnosis;
 KW treatment; prevention; cell proliferation; immune system disorder.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH 1..19
 FT Peptide /label= Signal_peptide
 FT Protein 20..470
 FT /label= Mature_ISMO-2
 FT Modified-site 120
 FT /note= "N-glycosylated"
 FT Modified-site 320

Fri Mar 9 16:49:01 2001

us-09-203-768a-2.rag

Page 10

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: March 9, 2001, 16:43:01 ; Search time 23.59 Seconds
(without alignments)
400.093 Million cell updates/sec

Title: US-09-203-768a-2
Perfect score: 748
Sequence: 1 MKHLMPFLLVAPRWVLSQ.....ARPHRYFDYWGQGLTVVSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	685.5	91.6	140	2 A49045	Ig heavy chain V r
2	641	85.7	140	2 S78052	Ig heavy chain pre
3	625.5	83.6	140	2 I37782	Ig variable region
4	589	78.7	139	2 S31586	Ig heavy chain V r
5	585	78.2	137	2 S31676	Ig heavy chain V r
6	584.5	78.1	147	2 S13519	Ig heavy chain V r
7	576	77.0	145	2 S78055	Ig heavy chain pre
8	571.5	76.4	146	1 G1H012	Ig heavy chain pre
9	571	76.3	126	2 S47010	Ig heavy chain V4.
10	570.5	76.3	139	2 S31596	Ig heavy chain V r
11	569.5	76.1	155	2 S31511	Ig heavy chain - h
12	563.5	75.3	155	2 S31512	Ig heavy chain - h
13	560.5	74.9	146	2 S09711	Ig heavy chain V r
14	558	74.6	231	2 B23746	Ig Fab region IV-J
15	554.5	74.1	143	2 B49028	Ig heavy chain V-I
16	550	73.5	116	2 B26340	Ig heavy chain pre
17	544.5	72.8	146	2 S09710	Ig heavy chain V r
18	539	72.1	118	2 A26340	Ig heavy chain pre
19	538	71.9	116	2 S18557	Ig heavy chain V r
20	535.5	71.6	140	2 A24770	hypothetical hybri
21	530.5	70.9	130	2 S31690	Ig heavy chain V r
22	530	70.9	122	2 J10047	Ig heavy chain V r
23	519	69.4	139	2 A41287	Ig heavy chain pre
24	518	69.3	97	2 S26898	Ig heavy chain V r
25	518	69.3	124	2 S31684	Ig heavy chain V r
26	514.5	68.8	114	2 I72667	cold agglutinin FS
27	514.5	68.8	130	2 S31673	Ig heavy chain V r
28	512.5	68.5	135	2 S78051	Ig heavy chain pre
29	512	68.4	143	2 B41287	Ig heavy chain pre

30	509	68.0	97	2 S14474	Ig heavy chain V r
31	508.5	68.0	137	2 S31585	Ig heavy chain V r
32	508	67.9	97	2 G34964	Ig heavy chain V-I
33	497.5	66.5	117	2 B34964	Ig heavy chain pre
34	490	65.5	97	2 S26805	Ig heavy chain V r
35	488	65.2	135	2 S31604	Ig heavy chain V r
36	483	64.6	97	2 S26806	Ig heavy chain V r
37	483	64.6	97	2 JH0428	Ig gamma chain V r
38	475	63.5	129	2 S44114	Ig heavy chain V r
39	472	63.1	97	2 S26808	Ig heavy chain V r
40	472	63.1	130	2 S30534	Ig heavy chain V r
41	466.5	62.4	121	2 S44113	Ig heavy chain V r
42	466	62.3	118	2 S24443	Ig heavy chain V r
43	464.5	62.0	123	2 S30530	Ig heavy chain V r
44	464	62.0	120	2 P0370	Ig mu chain precu
45	463.5	62.0	127	2 S19668	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Broquet, J.C.; Piller, F.; Rasseint, L.Z.; Labaume, S.; Silve
Eur. J. Immunol. 22, 1781-1788, 1992
A>Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes 1
A:Reference number: A49045; MUID:92324290
A:Accession: A49045
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <GR>
A:Cross-references: GB:S39381; NID:q250899; PID:AA22441.1; PID:q250900
A>Note: sequence extracted from NCBI backbone (NCBI:108088, NCBI:P:108089)
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: Immunoglobulin homology <IM>

Query Match 91.6%; Score 685.5; DB 2; Length 140;
Best Local Similarity 94.3%; Pred. No. 1.1e-54;
Matches 132; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

OY 1 MKHLMPFLLVAPRWVLSQVLOQMGAGLLKRPSTLSTCAVYGGSGYWSMIRPP 60
    |||||||
Db 1 MKHLMPFLLVAPRWVLSQVLOQMGAGLLKRPSTLSTCAVYGGSGYWSMIRPP 60
    |||||||

OY 61 GKGLEWIGEINHGSGTNPYSLKSVTTSVDTSKQFSLKSSVTAADTAVYYCAR-EIA 119
    |||||||
Db 61 GKGLEWIGEINHGSGTNPYSLKSVTTSVDTSKQFSLKSSVTAADTAVYYCAR-GRA 120
    |||||||

OY 120 ARPHRYFDYWGQGLTVVSS 139
    |||||||
Db 121 ATIVESFDYWGQGLTVVSS 140
    |||||||

RESULT 2
S78052
Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S23717
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAR>
A:Cross-references: EMBL:X54441; NID:q37815; PID:CAA38308.1; PID:q930118
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notk
```

Int. Immunol. 3, 865-875, 1991
 A>Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity B cell antigen receptors from a human patient.
 A:Reference number: S23716; MUID:92031262
 A:Accession: S23717
 A:Molecule type: mRNA
 A:Residues: 15-111 <HMM>
 A:Cross-references: EMBL:X54441
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
 F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
 F:29-111/Domain: immunoglobulin homology <IMM>

Query Match 85.7%; Score 641; DB 2; Length 140;
 Best Local Similarity 88.7%; Pred. No. 1.1e-50;
 Matches 126; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

OY 6 FLLVLAAPRWVLSQVLOQMGAGILKPSSETLSITCAVYGGSGFYWSMIRPPGKLE 65
 |||
 DB 1 KHLVLAAPRWVLSQVLOQMGAGILKPSSETLSITCAVYGGSGFYWSMIRPPGKLE 60
 OY 66 WIGELNHSGSTNPNPSLKSRVTISVDTSKNPFSLKSSVTADTAAYYCAR-----E 117
 |||
 DB 61 WIGELNHSGSTNPNPSLKSRVTISVDTSKNPFSLKSSVTADTAAYYCARGGSVLRLE 120
 OY 118 IAPRHRFDYWGOGTLVTVSS 139
 |||
 DB 121 WLLYP--AFDYWGOGTLVTVSS 140

RESULT 3

Ig variable region (VDJ) (clone T23-9) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
 C:Accession: I37782; S25476
 R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
 Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
 A>Title: Somatic diversification in the heavy chain variable region genes expressed by B cells from a human patient.
 A:Reference number: A6876; MUID:94119917
 A:Accession: I37782
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-140 <RES>
 A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:46-128/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 625.5; DB 2; Length 140;
 Best Local Similarity 86.4%; Pred. No. 2.6e-49;
 Matches 121; Conservative 6; Mismatches 12; Indels 1; Gaps 1;
 OY 1 KHLVLAAPRWVLSQVLOQMGAGILKPSSETLSITCAVYGGSGFYWSMIRPP 60
 |||
 DB 1 KHLVLAAPRWVLSQVLOQMGAGILKPSSETLSITCAVYGGSGFYWSMIRPP 60
 OY 61 GKLEWIGELNHSGSTNPNPSLKSRVTISVDTSKNPFSLKSSVTADTAAYYCARLEIAA 120
 |||
 DB 61 GKLEWIGELNHSGSTNPNPSLKSRVTISVDTSKNPFSLKSSVTADTAAYYCARHNS 120
 OY 121 RPHY--FDYWGOGTLVTVSS 139
 |||
 DB 121 SWYGRYFDYWGOGTLVTVSS 140

RESULT 4

S31586
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31586
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
 Submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
 A:Reference number: S31585
 A:Accession: S31586
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-139 <CU>
 A:Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 589; DB 2; Length 139;
 Best Local Similarity 82.9%; Pred. No. 4.9e-46;
 Matches 115; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

OY 1 KHLVLAAPRWVLSQVLOQMGAGILKPSSETLSITCAVYGGSGFYWSMIRPP 60
 |||
 DB 1 KHLVLAAPRWVLSQVLOQMGAGILKPSSETLSITCAVYGGSGFYWSMIRPP 60
 OY 61 GKLEWIGELNHSGSTNPNPSLKSRVTISVDTSKNPFSLKSSVTADTAAYYCARLEIAA 120
 |||
 DB 61 GKLEWIGELNHSGSTNPNPSLKSRVTISVDTSKNPFSLKSSVTADTAAYYCARGLG 120
 OY 121 RPHYFDYWGOGTLVTVSS 139
 |||
 DB 121 IRRGAFDIDWGOGTLVTVSS 139

RESULT 5

Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31676
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
 Submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
 A:Reference number: S31585
 A:Accession: S31676
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-137 <CU>
 A:Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 585; DB 2; Length 137;
 Best Local Similarity 82.9%; Pred. No. 1.1e-45;
 Matches 116; Conservative 4; Mismatches 16; Indels 4; Gaps 2;
 OY 1 KHLVLAAPRWVLSQVLOQMGAGILKPSSETLSITCAVYGGSGFYWSMIRPP 60
 |||
 DB 1 KHLVLAAPRWVLSQVLOQMGAGILKPSSETLSITCAVYGGSGFYWSMIRPP 60
 OY 61 GKLEWIGELNHSGSTNPNPSLKSRVTISVDTSKNPFSLKSSVTADTAAYYCARLEIAA 120
 |||
 DB 61 GKLEWIGELNHSGSTNPNPSLKSRVTISVDTSKNPFSLKSSVTADTAAYYCARDD--- 117
 OY 121 RPHY--FDYWGOGTLVTVSS 139
 |||
 DB 118 APLMYGMDYWGOGTLVTVSS 137

RESULT 6

S13519
 Ig heavy chain V region precursor - human
 C:Species: Homo sapiens (man)

Query Match 76.3%; Score 571; DB 2; Length 126;
 Best Local Similarity 87.3%; Pred. No. 1.8e-44;
 Matches 110; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

OY 20 OYLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPPGKLEWIGELINHSSTNN 79
 |||||
 DB 1 OYLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPPGKLEWIGELINHSSTNN 60
 OY 80 PSLKSVTISVDTSKNOFSKLSSVTAAADTAVYYCAR-----ETIARRHRYFDYWGQGT 133
 |||||
 DB 61 PSLKSVTISVDTSKNOFSKLSSVTAAADTAVYYCARGGCCPKKACCYTRKNFDPWGQGT 120
 OY 134 LVTYSS 139
 |||||
 DB 121 LVTYSS 126

RESULT 10

S31696

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)
 C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31696
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelier, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31696
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-139 <CU>
 A:Cross-references: EMBL:Z14194; NID:g30975; PIDN:CAA7B65.1; PID:g30976
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:34-116/Domain: Immunoglobulin homology <IMM>

Query Match 76.3%; Score 570.5; DB 2; Length 139;
 Best Local Similarity 81.5%; Pred. No. 2.2e-44;
 Matches 110; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

OY 1 MKHLWFFLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPP 60
 |||||
 DB 1 MKHLWFFLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCTVSGSISYWSWIRPPA 60
 OY 61 GKLEWIGELINHSSTNNPSLSKRVYISVDTSKNOFSKLSSVTAAADTAVYYCAR-EIA 119
 |||||
 DB 61 AKGLEWIGITVYSGSTNNPSLSKRVYISVDTSKNOFSKLSSVTAAADTAVYYCARGGIG 120
 OY 120 AARHRYFDYWGQGT 134
 ::|||
 DB 121 LMGDKWIDYWGQGT 135

RESULT 11

S31511

Ig heavy chain - human

C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S31511
 R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
 submitted to the EMBL Data Library, December 1992
 A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
 A:Reference number: S31509
 A:Accession: S31511
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-155 <CH>
 A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin

F:47-129/Domain: Immunoglobulin homology <IMM>

Query Match 76.1%; Score 569.5; DB 2; Length 155;
 Best Local Similarity 77.8%; Pred. No. 3.1e-44;
 Matches 112; Conservative 7; Mismatches 18; Indels 7; Gaps 2;

OY 1 MKHLWFFLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPP 60
 |||||
 DB 14 MKHLWFFLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCTVSGSISYWSWIRPP 73
 OY 61 GKLEWIGELINHSSTNNPSLSKRVYISVDTSKNOFSKLSSVTAAADTAVYYCAR-EIA 120
 |||||
 DB 74 GKLEWIGITVYSGSTNNPSLSKRVYISVDTSKNOFSKLSSVTAAADTAVYYCAR--CG 131
 OY 121 RHRFYD-----WGQGLVTYSS 139
 ::|||
 DB 132 GISSWYDYGMVWGQGTVTYSS 155

RESULT 12

S31512

Ig heavy chain - human

C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S31512
 R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
 submitted to the EMBL Data Library, December 1992
 A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA a
 A:Reference number: S31509
 A:Accession: S31512
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-155 <CH>
 A:Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin
 F:47-129/Domain: Immunoglobulin homology <IMM>

Query Match 75.3%; Score 563.5; DB 2; Length 155;
 Best Local Similarity 78.9%; Pred. No. 1.1e-43;
 Matches 112; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

OY 1 MKHLWFFLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCAVYGGSFSGYWSWIRPP 60
 |||||
 DB 14 MKHLWFFLLVAPRWVLSQVLOQMGAGLLKPSFTLSLTCTVSGSISYWSWIRPP 73
 OY 61 GKLEWIGELINHSSTNNPSLSKRVYISVDTSKNOFSKLSSVTAAADTAVYYCAR--EI 118
 |||||
 DB 74 GKLEWIGITVYSGSTNNPSLSKRVYISVDTSKNOFSKLSSVTAAADTAVYYCARGGGI 133
 OY 119 AARHRYFDYWGQGLVTYSS 139
 ::|||
 DB 134 SSMVYVYGMVWGQGTVTYSS 155

RESULT 13

S09711

Ig heavy chain V region - human

C:Species: Homo sapiens (man)
 C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 C:Accession: S09711
 R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coatswell, J.
 Biochem. J. 268, 135-140, 1990
 A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domain
 A:Reference number: S09710; MUID:90262535
 A:Accession: S09711
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-146 <HUG>
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; Immunoglobulin

Fri Mar 9 16:49:07 2001

us-09-203-768a-2.rpr

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:43:06 ; Search time 14.74 Seconds
(without alignments)
304.537 Million cell updates/sec

Title: US-09-203-768A-2

Perfect score: 748
Sequence: 1 MKHLMFLLVAAAPRWLSQ.....ARPHRYFDYWGQGLTVYSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571.5	76.4	146	1	HV21_HUMAN
2	411.5	55.0	129	1	HV2F_HUMAN
3	408	54.5	137	1	HV46_MOUSE
4	397.5	53.1	117	1	HV2G_HUMAN
5	370	49.5	116	1	HV60_MOUSE
6	369.5	49.4	144	1	HV43_MOUSE
7	359.5	48.1	113	1	HV47_MOUSE
8	359.5	48.1	135	1	HV01_XENLA
9	343	45.9	116	1	HV01_MOUSE
10	330	44.1	139	1	HV07_MOUSE
11	329	44.0	137	1	HV11_MOUSE
12	328	43.9	119	1	HV37_MOUSE
13	326.5	43.6	117	1	HV62_MOUSE
14	326	43.6	119	1	HV38_MOUSE
15	325	43.4	119	1	HV40_MOUSE
16	323.5	43.2	138	1	HV48_MOUSE
17	322	43.0	122	1	HV3G_HUMAN
18	321	42.9	136	1	HV01_XENLA
19	317.5	42.4	117	1	HV41_MOUSE
20	316.5	42.3	118	1	HV33_MOUSE
21	316.5	42.3	142	1	HV01_RAT
22	316	42.2	115	1	HV44_MOUSE
23	310	41.4	120	1	HV50_MOUSE
24	306.5	41.0	123	1	HV22_MOUSE
25	305.5	40.8	121	1	HV01_MOUSE
26	304	40.6	116	1	HV45_MOUSE
27	303.5	40.6	115	1	HV3Z_HUMAN
28	303.5	40.6	117	1	HV42_MOUSE
29	302.5	40.4	117	1	HV13_MOUSE
30	302.5	40.4	140	1	HV02_MOUSE
31	300.5	40.2	117	1	HV12_MOUSE
32	300.5	40.2	121	1	HV34_HUMAN
33	299	40.0	147	1	HV2H_HUMAN

34	297	39.7	120	1	HV2B_HUMAN
35	296	39.6	118	1	HV51_MOUSE
36	295.5	39.5	120	1	HV03_MOUSE
37	295.5	39.5	123	1	HV18_MOUSE
38	295.5	39.5	123	1	HV19_MOUSE
39	294.5	39.4	123	1	HV23_MOUSE
40	293	39.2	122	1	HV2C_HUMAN
41	292.5	39.1	119	1	HV2C_HUMAN
42	290.5	38.8	117	1	HV04_MOUSE
43	288.5	38.6	117	1	HV17_MOUSE
44	288	38.5	122	1	HV20_MOUSE
45	287.5	38.4	116	1	HV36_MOUSE

ALIGNMENTS

RESULT	ID	Query Match	Score	DB 1	Length	DB 2
1	HV21_HUMAN	76.4%	571.5	DB 1	146	
AC	P06331	Best Local Similarity	78.1%	Pred. No. 1e-47		
DT	01-JAN-1988 (Rel. 06, Last sequence update)	Matches 114; Conservative	5;	Mismatches 20;	Indels 7;	Gaps 2;
DT	01-JAN-1988 (Rel. 06, Last sequence update)					
DE	IG HEAVY CHAIN V-II REGION ARH-77 PRECURSOR.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	MEDLINE-85205332; PubMed-3922855;					
RX	Kudo A., Ishihara T., Nishimura Y., Watanabe T.;					
RT	"A cloned human immunoglobulin heavy chain gene with a novel direct-repeat sequence in 5' flanking region."					
RL	Gene 33:181-189(1985).					
DR	PIR; A02101; G1H0H2.					
DR	HSSP; P01825; 7FAB.					
DR	INTERPRO; IPR003006; .					
DR	PFAM; PF00047; 1g; 1.					
KW	Immunoglobulin V region; Signal.					
FT	SIGNAL					
FT	CHAIN					
FT	DOMAIN					
FT	DOMAIN					
FT	DOMAIN					
FT	DISULFID					
FT	NON_TER					
SQ	SEQUENCE					
Query Match						
Best Local Similarity						
Matches 114; Conservative						
5;						
Mismatches 20;						
Indels 7;						
Gaps 2;						
1	MKHLMFLLVAAAPRWLSQVLQOWAGAGLRKPESTLSITCAVYGGSGYWSWIRP 59					
1	MKHLMFLLVAAAPRWLSQVLQOWAGAGLRKPESTLSITCAVYGGSGYWSWIRP 60					
60	PKGLEWIGELINSGSNVNPISLRSRTISVDTSKNQPSIKLSSTVTAADVAAYYCAREIA 119					
61	PKGLEWIGELINSGSNVNPISLRSRTISVDTSKNQPSIKLSSTVTAADVAAYYCAREIA 120					
120	ARPHRYFDY-----WGQGLTVYSS 139					
121	RGGMNDVDYTYGMDVWGQGLTVYSS 146					
RESULT						
2	HV2F_HUMAN	STANDARD;	PRT;	129 AA.		
ID	HV2F_HUMAN					
AC	P01824;					
DT	21-JUL-1986 (Rel. 01, Created)					
DT	21-JUL-1986 (Rel. 01, Last sequence update)					

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION WAH.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE:
 RX MEDLINE=8222235; PubMed=6806818;
 RA Takahashi N., Tetaert D., Debuire B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 immunoglobulin D."; Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 RL CC
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 PROTEIN.
 DR PIR: A02099; D2H0WA.
 DR HSSP: P01825; 7FAB.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 DR IMMUNOGLOBULIN V region.
 FT NON_TER 129 129
 FT SEQUENCE 129 AA; 14117 MW; D5D53D47ABE51319 CRC64;

Query Match 55.0%; Score 411.5; DB 1; Length 129;
 Best Local Similarity 62.1%; Pred. No. 1.4e-32;
 Matches 82; Conservative 14; Mismatches 21; Indels 15; Gaps 3;

QY 20 QVQLQOQWAGLTKRPSFLSLTCAVYGSF--SGYWSMIRPGPKGLWGLGELNHSSTN 77
 DB 1 RLQLQSGPLVPSFLSLTCAVYGSFIRRTGYWGMWIMPPKGLWGLGELNHSSTN 60
 QY 78 YNLSLRVTISVDTSKNPSFLSLTCAVYGSFIRRTGYWGMWIMPPKGLWGLGELNHSSTN 127
 DB 61 YNLSLRVTISVDTSKNPSFLSLTCAVYGSFIRRTGYWGMWIMPPKGLWGLGELNHSSTN 117
 QY 128 YWGQGLTVTVSS 139
 DB 118 YWGQGLTVTVSS 129

RESULT 3
 HV46_MOUSE STANDARD; PRT; 137 AA.
 ID HV46_MOUSE
 AC P01822;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MOPC 315 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89238351; PubMed=2497341;
 RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
 RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
 gene segment."; Mol. Immunol. 26:431-434(1989).
 RL CC
 CC -1- Immunol. 26:431-434(1989).
 RN [2]
 RP SEQUENCE OF 1-31.
 RX MEDLINE=78094475; PubMed=414225;
 RA Jilka R.L., Pestka S.;
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse
 immunoglobulin heavy chain."; Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
 RN [3]
 RP SEQUENCE OF 1-21.
 RX MEDLINE=79148758; PubMed=428562;
 RA Schechter I., Wolf O., Zemel R., Burstein Y.;
 RT "Structure and function of immunoglobulin genes and precursors."; Fed. Proc. 38:1833-1845(1979).
 RL [4]
 RP SEQUENCE OF 19-136.

RX MEDLINE=74170779; PubMed=4524622;
 RA Francis S.H., Leslie R.G.O., Hood L., Eisen H.N.;
 RT "Amino-acid sequence of the variable region of the heavy (alpha)
 chain of a mouse myeloma protein with anti-hapten activity."; Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
 RN [5]
 RP REVISION TO 53.
 RX MEDLINE=77244979; PubMed=268248;
 RA Hood L., Margolis M.N., Givol D., Zakut R.;
 RT Unpublished results, cited by:
 RL Padian E.A., Davies D.R., Pecht I., Givol D., Wright C.;
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
 RL CC
 CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
 CC
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CC EMBL: M27638; AAA61337.1; -
 DR EMBL: X07880; CAA30727.1; -
 DR PIR: P0102; AVM335.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19; 1.
 DR IMMUNOGLOBULIN V region; Signal.
 KW SIGNAL 1 18
 FT CHAIN 19 137
 FT DOMAIN 19 48 IG HEAVY CHAIN V REGION MOPC 315.
 FT DOMAIN 49 54 FRAMEWORK 1.
 FT DOMAIN 55 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 84 FRAMEWORK 2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 85 116 FRAMEWORK 3.
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 127 137 FRAMEWORK 4.
 FT DISULFID 40 114 BY SIMILARITY.
 FT CONFLICT 15 15 G -> GG (IN CAA30727).
 FT CONFLICT 15 15 G -> H (IN REF. 2).
 FT CONFLICT 77 78 GY -> YG (IN REF. 4).
 FT CONFLICT 102 102 N -> D (IN REF. 4).
 FT CONFLICT 123 123 MISSING (IN REF. 4).
 FT NON_TER 137 137
 FT SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;

Query Match 54.5%; Score 408; DB 1; Length 137;
 Best Local Similarity 60.3%; Pred. No. 3.3e-32;
 Matches 85; Conservative 18; Mismatches 32; Indels 6; Gaps 4;

QY 1 MKHLRFLLVAPRNVLSVQLOQWAGLTKRPSFLSLTCAVYGSF--SGYWSMIRPG 59
 DB 1 MKVLSLYLLTAIP-CIMSVDVQLQSGPLVPSFLSLTCAVYGSFIRRTGYWGMWIMPPKGLWGLGELNHSSTN 59
 QY 60 PGKGLMIGELINSGSTNPSFLSLTCAVYGSFIRRTGYWGMWIMPPKGLWGLGELNHSSTN 119
 DB 60 PGKGLMIGELINSGSTNPSFLSLTCAVYGSFIRRTGYWGMWIMPPKGLWGLGELNHSSTN 117
 QY 120 ARPH-RYFDYWGQGLTVTVSS 139
 DB 118 -NDHLYFDYWGQGLTVTVSS 137

RESULT 4
 HV2G_HUMAN STANDARD; PRT; 117 AA.
 ID HV2G_HUMAN
 AC P01825;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION NEMM.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE-7242302; PubMed-407927;
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.;
 RT "Amino acid sequence of the VH region of a human myeloma
 immunoglobulin (IgG New).";
 RL Biochemistry 16:3412-3420(1977).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE-78066916; PubMed-618887;
 RA Saul F.A., Amzel L.M., Poljak R.J.;
 RT "Preliminary refinement and structural analysis of the Fab fragment
 from human immunoglobulin new at 2.0-A resolution.";
 RL J. Biol. Chem. 253:585-597(1978).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 PROTEIN.
 DR PIR: A02100; G1H0NM.
 DR PDB: 7EAB; 31-JAN-94.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19: 1.
 KW Immunoglobulin V region; 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT STRAND 3 7
 FT 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 57 59
 FT HELIX 61 63
 FT TURN 64 66
 FT STRAND 67 72
 FT TURN 73 76
 FT STRAND 77 82
 FT HELIX 87 89
 FT STRAND 91 98
 FT STRAND 104 107
 FT STRAND 111 115
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 53.1%; Score 397.5; DB 1; Length 117;
 Best Local Similarity 64.2%; Pred. No. 2.8e-31;
 Matches 77; Conservative 19; Mismatches 21; Indels 3; Gaps 1;

QY 20 QVLOQMGGLKPSFELSTLCAYVGGSGFYWMTROPKGLWIGINSGSTNYN 79
 DB 1 QVLEQSGGLVPSQTLSTCTVSGSTFSDNYTWKPGKGLWIGYFVHGTSDDT 60
 QY 80 PSIKSHVTISVDTSKNOFSIKLSVTAAADPAVYCCAREIARPHRYEDYGGGTLVTSS 139
 DB 61 TPLRSVTHMLVDTSKNOFSIKLSVTAAADPAVYCCARNLIA---GCCIDWGGGSLVTSS 117

RESULT 5
 HY60_MOUSE STANDARD; PRT; 116 AA.
 AC P18531;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION M315 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/CJ;
 RX MEDLINE-89279149; PubMed-2499654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 DR PIR: J0509; HVMS31.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19: 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 116
 FT DOMAIN 19 48 IG HEAVY CHAIN V REGION M315.
 FT DOMAIN 49 53 FRAMEWORK 1.
 FT DOMAIN 54 67 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 68 84 FRAMEWORK 2.
 FT DOMAIN 85 116 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 40 114 FRAMEWORK 3.
 FT NON_TER 116 116 BY SIMILARITY.
 SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 49.5%; Score 370; DB 1; Length 116;
 Best Local Similarity 64.1%; Pred. No. 1.1e-28;
 Matches 75; Conservative 15; Mismatches 25; Indels 2; Gaps 2;

QY 1 MKHLMEFLLVAPRWLSQVLOQMGGLKPSFELSTLCAYVGGSGFYWMTROP 59
 DB 1 MKVLSLYLLTALP-GLISVLOESGGLVKPSQSLCTSVGISTGYSITGWNWTRQP 59
 QY 60 PGKGLWIGINSGSTNYNPSIKSRVTSVDTSKNOFSIKLSVTAAADPAVYCCAR 116
 DB 60 PGKLEWNGYISDGSNNYNPSIKSRISITRDTSKNOFPLKINSVTEDPATYTCAR 116

RESULT 6
 HY43_MOUSE STANDARD; PRT; 144 AA.
 AC P01819;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-8102133; PubMed-6774258;
 RA Sakano H., Makl R., Kurosawa Y., Roeder W., Tonegawa S.;
 RT "Two types of somatic recombination are necessary for the generation
 of complete immunoglobulin heavy-chain genes.";
 RL Nature 286:676-683(1980).
 CC -I- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
 DIFFERENTIATED GENE ISOLATED FROM A MYELOMA THAT SECRETES IGG2B.
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 CC EMBL: J00491; AAA38121.1; -
 CC EMBL: V00768; CAA24149.1; -
 CC PIR: A02094; G2MS14.
 CC INTERPRO: IPR003006; -
 CC PFAM: PF00047; 19: 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 144 IG HEAVY CHAIN V REGION MOPC 141.


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DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 IG HEAVY CHAIN V REGION 1B43.
FT DOMAIN 19 48 FRAMEWORK 1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 54 67 FRAMEWORK 2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 13158 MW; 1CB547253681FF74 CRC64;

Query Match
Best Local Similarity 45.9%; Score 343; DB 1; Length 116;
Matches 71; Conservative 16; Mismatches 28; Indels 2; Gaps 2;

QY 1 MKHLWFFLLVAAPRWLVSOVLQOQAGLLKPESETLTCAYVGGSF-SGYYSWMIROP 59
D 1 MRVLILLCLFTAPP-GILSDVQIQESGPDLYKPSQSLSLTCVTVTGYSTGSGMHWIRPF 59
DB 60 PGKLEMGVIHYSGMTSYNPSLKSRISTRDSKNOFFQLNSVTEDEYATYTCAR 116
QY 60 PGKLEMGVIHYSGMTSYNPSLKSRISTRDSKNOFFQLNSVTEDEYATYTCAR 116
D 60 PGKLEMGVIHYSGMTSYNPSLKSRISTRDSKNOFFQLNSVTEDEYATYTCAR 116
DB 60 PGKLEMGVIHYSGMTSYNPSLKSRISTRDSKNOFFQLNSVTEDEYATYTCAR 116

RESULT 10
HVO7_MOUSE STANDARD; PRT; 139 AA.
ID HVO7_MOUSE
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION BI-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RX Baltsell A.L.M., Paskind M., Imanishi-Kari T., Rajewsky K.,
RX Baltimore D.;
RA "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE BI-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL: J00529; AAA38170.1; -
CC PIR: A02034; MHMS18.
CC INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION BI-8/186-2.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT NON_TER 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.

```

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FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57D4FDC09F465 CRC64;

Query Match
Best Local Similarity 44.1%; Score 330; DB 1; Length 139;
Matches 67; Conservative 22; Mismatches 42; Indels 2; Gaps 2;

QY 8 LLLVAAPRWLVSOVLQOQAGLLKPESETLTCAYVGGSGYYSWMIROPKGLEMI 67
D 8 LFLAATRTGVHSOVOLQOQAGELVKGASVYKSCAKSGITFTSYMMHWKQGRGKLEMI 67
DB 68 GRDPPNSGGRKYNKMKRSKATLVDPKPSRYAVQMSLSLSEDSAYVYTCAR-YYYGSSYF 126
QY 127 DYWGQGLTVYSS 139
D 127 DYWGQGLTVYSS 139
DB 127 DYWGQGLTVYSS 139

RESULT 11
HVL1_MOUSE STANDARD; PRT; 137 AA.
ID HVL1_MOUSE
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RX Baltsell A.L.M., Paskind M., Imanishi-Kari T., Rajewsky K.,
RX Baltimore D.;
RA "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -I- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00539; AAA38172.1; -
CC PIR: A02038; G2MS43.
CC INTERPRO: IPR003006; -
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BFA4B8BC9 CRC64;

Query Match
44.0%; Score 329; DB 1; Length 137;

```

Best Local Similarity 49.6%; Pred. No. 1.1e-24;
Matches 66; Conservative 22; Mismatches 41; Indels 4; Gaps 2;

OY 8 LILVAPRWLISQVLOQMGAGLLKPSFTSLTCAVYGGSGFSGYWMSWIRPPGKGLWEI 67
DB 8 LFLAAATGATGHSVOVLOQPGAEFTVKGASVYKLSCKASGFTSYLHMWVORGRGLEWI 67
OY 68 GEIN-HSGSTNPNPSLKSRVITSDVTSKNOFSLKSSVTADTAVYCARREIARPHRYF 126
DB 68 GRIDPNSGGTVEHFRSKATLTIDKPSSTAVYVQSLSTSEDSAVYVCAR---YRLGRYF 124
OY 127 DWGCGTLTVSS 139
DB 125 DWGCGTLTVSS 137

RESULT 12
HV37_MOUSE
ID HV37_MOUSE STANDARD; PRT; 119 AA.

AC P01807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION X44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudnikoff S., Kruttsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
its potential role in generating diversity in
complementarity-determining regions."
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
THAT BINDS GALACTAN.
CC PIR: A02077; AVMSX4.
DR HSSP: P01810; 2FBJ.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g.1.
KW Immunoglobulin V region.
FT NON_TER 119
SQ SEQUENCE 119 AA; 13246 MW; BC34FC8F31CDA1B3 CRC64;

Query Match 43.9%; Score 328; DB 1; Length 119;
Best Local Similarity 54.5%; Pred. No. 1.2e-24;
Matches 66; Conservative 17; Mismatches 34; Indels 4; Gaps 2;

OY 20 OVOLQMGAGLLKPSFTSLTCAVYGGSGFSGYWMSWIRPPGKGLWEIINHSST-NY 78
DB 1 EVKLLSGGGLVOPGGSLKSLCAASGFDSRYWMSWVROAPGKGLWEIINDSSTIN 60
OY 79 NPSLKSRTVSDVTSKNOFSLKSSVTADTAVYCARREIARPHRYFDWCGTLTVTS 138
DB 61 TPLSKKFTISRMAKNTLYLQMSKYRSEDFTALYCAR---LHYGYAAYWGGTLTVTS 117
OY 139 S 139
DB 118 A 118

RESULT 13
HV62_MOUSE
ID HV62_MOUSE STANDARD; PRT; 117 AA.
AC P18533;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 733 PRECURSOR.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response."
J. Exp. Med. 169:2007-2019(1989).
DR PIR: J0510; HVMS73.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g.1.
KW Immunoglobulin V region; Signal.
FT CHAIN 19 117 IG HEAVY CHAIN V REGION 733.
FT DISULFID 40 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13223 MW; 1595517827F976BE CRC64;

Query Match 43.6%; Score 326.5; DB 1; Length 117;
Best Local Similarity 57.6%; Pred. No. 1.6e-24;
Matches 68; Conservative 15; Mismatches 32; Indels 3; Gaps 2;

OY 1 MKHLMFLLVAPRWVLSQVLOQMGAGLLKPSFTSLTCAVYGGSGFS--GYWMSWIR 58
DB 1 MKMFTLLYLLTVVP-GILSDVQLOESGPGIVKPSGSIATLCYTGTGSIITGNRMWM 59
OY 59 PEGKGLWEIINHSSTNPNPSLKSRVITSDVTSKNOFSLKSSVTADTAVYCAR 116
DB 60 FPGNKLEWIGYIYSAITSYNPSKSRVITSDVTSKNOFSLKSSVTADTAVYCAR 117

RESULT 14
HV38_MOUSE
ID HV38_MOUSE STANDARD; PRT; 119 AA.

AC P01808;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION T601.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudnikoff S., Kruttsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
its potential role in generating diversity in
complementarity-determining regions."
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
THAT BINDS GALACTAN.
CC PIR: A02078; AVMS76.
DR HSSP: P01810; 2FBJ.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g.1.
KW Immunoglobulin V region.
FT NON_TER 119
SQ SEQUENCE 119 AA; 13169 MW; BC38CC84E6EA00E8 CRC64;

Query Match 43.6%; Score 326; DB 1; Length 119;
Best Local Similarity 54.5%; Pred. No. 1.8e-24;
Matches 66; Conservative 16; Mismatches 35; Indels 4; Gaps 2;

OY 20 OVOLQMGAGLLKPSFTSLTCAVYGGSGFSGYWMSWIRPPGKGLWEIINHSST-NY 78
DB 1 EVKLLSGGGLVOPGGSLKSLCAASGFDSRYWMSWVROAPGKGLWEIINDSSTIN 60

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: March 9, 2001, 16:43:41 ; Search time 38.3 seconds
(without alignments)
425.376 Million cell updates/sec

Title: US-09-203-768A-2
Perfect score: 748
Sequence: 1 MKHLMPFLLVAAFRWVLSQ.....ARPHRYPDYMGQGLTVTVSS 139

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	552	73.8	150	4	095973	095973 homo sapien
2	490.5	65.6	119	4	090L73	090L73 homo sapien
3	371	49.6	122	4	090L75	090L75 homo sapien
4	354.5	47.4	298	11	090YF0	090YF0 mus musculi
5	328.5	43.9	82	4	075725	075725 homo sapien
6	314	42.0	122	4	090L84	090L84 homo sapien
7	313.5	41.9	121	4	090L96	090L96 homo sapien
8	312.5	41.8	117	11	090XF0	090XF0 mus musculi
9	312	41.7	78	4	075739	075739 homo sapien
10	308.5	41.2	117	11	090XE9	090XE9 mus musculi
11	308.5	41.2	131	4	090L88	090L88 homo sapien
12	305.5	40.8	113	4	090L90	090L90 homo sapien
13	305	40.8	124	4	090L92	090L92 homo sapien
14	304.5	40.7	121	4	090L71	090L71 homo sapien
15	304	40.6	147	4	09Y509	09Y509 homo sapien
16	296.5	39.6	75	4	075743	075743 homo sapien
17	296.5	39.6	118	4	090L74	090L74 homo sapien
18	295	39.4	118	4	090L72	090L72 homo sapien
19	292.5	39.1	125	4	090L95	090L95 homo sapien

20	291	38.9	118	4	090L91	090L91 homo sapien
21	288.5	38.6	116	4	090L93	090L93 homo sapien
22	287	38.4	118	11	092L14	092L14 mus musculu
23	286	38.2	437	11	09R1A4	09R1A4 mus musculu
24	284.5	38.0	119	4	090L94	090L94 homo sapien
25	283	37.8	110	11	090L77	090L77 mus musculu
26	278.5	37.2	88	4	075737	075737 homo sapien
27	276	36.9	116	4	090L89	090L89 homo sapien
28	274	36.6	109	11	090L75	090L75 mus musculu
29	269.5	36.0	117	11	092L16	092L16 mus musculu
30	266.5	35.6	109	11	090L85	090L85 mus musculu
31	266	35.6	124	6	090N06	090N06 oryctolagus
32	265	35.4	114	11	090L81	090L81 mus musculu
33	264.5	35.3	150	4	09Y298	09Y298 homo sapien
34	264	35.3	124	6	090N04	090N04 oryctolagus
35	259.5	34.7	112	4	090GP3	090GP3 homo sapien
36	256.5	34.3	95	4	090LB6	090LB6 homo sapien
37	256.5	34.3	157	4	095978	095978 homo sapien
38	255.5	34.2	104	4	090L87	090L87 homo sapien
39	245	32.8	97	4	043234	043234 homo sapien
40	238	31.8	110	11	090L83	090L83 mus musculu
41	224.5	30.0	77	4	075741	075741 homo sapien
42	223.5	29.9	102	11	090L79	090L79 mus musculu
43	218	29.1	416	4	09NP6	09NP6 homo sapien
44	216.5	28.9	78	4	075730	075730 homo sapien
45	208	27.8	80	4	075727	075727 homo sapien

ALIGNMENTS

RESULT 1
ID 095973 PRELIMINARY: PRT: 150 AA.
AC 095973;
DT 01-MAY-1999 (TREMBLrel, 10, Created)
DT 01-MAY-1999 (TREMBLrel, 10, last sequence update)
DT 01-MAY-2000 (TREMBLrel, 13, last annotation update)
DE V44 HEAVY CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).
GN IGM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Suh C.-H., Song C.-H., Lee C.-H., Lee S.-K.;
RT "Clonal proliferation of Igm secreting B cell in the synovium of
RT Benecet's patient with arthritis."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF103795; AAC79084.1; -
DR HSSP; P01825; 7FAB.
DR INTERPRO: IPR003006; -
DR PFM; PF00047; 19; 1.
KW Signal.
FT SIGNAL. 1 19
FT CHAIN 20 >150 V44 HEAVY CHAIN VARIABLE REGION.
FT NON_TER 150
SQ SEQUENCE 150 AA; 16315 MW; 85664ED04938AA7C9 CRC64;

Query Match 73.8%; Score 552; DB 4; Length 150;
Best Local Similarity 76.8%; Pred. No. 5.8e-49;
Matches 109; Conservative 11; Mismatches 14; Indels 8; Gaps 3;

QY 1 MKHLMPFLLVAAFRWVLSQVLOQNGAGLTKPSEFLSLTCAYVGGSF--GYWGMIRQ 58
DB 1 MKHLMPFLLVAAFRWVLSQVLOQNGAGLTKPSEFLSLTCAYVGGSF--GYWGMIRQ 60
QY PPKGGEWGEINHGSGSTNNPSLKSRTVTSVDTSKNPSLKSSTVADTAVYCAR-E 117
DB 61 PPKGGEWGEINHGSGSDYNNPSLKSRTVTSVDTSKNPSLKSSTVADTAVYCARLG 120

```
Qy      118 IARPHRYFDYWGQGLTVVSS    139  
          : | ||| ||| |||  
Db      121 MGA-----FDFWGHGTMVTVSS    137
```

RESULT	2		
09UL73			
ID	09UL73	PRELIMINARY;	PRT; 119 AA.
AC	09UL73;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT	01-JUN-2000 (TrEMBLrel. 14, Last annotation update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)		
OS	Homo sapiens (human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,		
RA	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal		
RT	fetus.";		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL; AF035041; AAD56277.1; -		
DR	INTERPRO; IPR003006; -		
DR	PFAM; PF00047; 1g. 1.		
FT	NON_TER 1 1		
FT	NON_TER 119 119		
QO	SEQUENCE 119 AA: 13219 MW; 1BDB86F6420EA0BE CRC64;		

RESULT	3
09UL75	
ID	PRELIMINARY; PRT; 122 AA.
AC	09UL75;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE	MYOSIN-II-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)
OS	homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI	TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98277139; PubMed=9614934;
RA	Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA	Young D.C.;
RT	"Myosin-II-reactive autoantibodies in rheumatic carditis and normal
RT	fetus.";
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).
DR	EMBL; AF035039; AAD56275.1; -.
DR	INTERPRO; IPR003006; -.
PFAM;	PF00047; 19; 1.
FT	NON_TER
FT	1 122
FT	1 122
SEQUENCE	122 AA: 13719 MW; 56CB0612586A5529 CRC64;

[illegible]

Q90YF0	4	PRELIMINARY;	PRT;	298 AA.
ID	Q90YF0			
AC	Q90YF0			
DT	01-MAY-2000 (TREMBLrel, 13, Created)			
DT	01-MAY-2000 (TREMBLrel, 13, last sequence update)			
DT	01-OCT-2000 (TREMBLrel, 15, last annotation update)			
DE	CN 8 SCFV.			
GN	CN 8.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RC	SEQUENCE FROM N.A.			
RP	SPRAIN-BALB/C; TISSUE=SPLEEN;			
RA	Shinohara N., Demura T., Fukuda H.;			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RP	SPRAIN-BALB/C; TISSUE=SPLEEN;			
RA	Shinohara N., Demura T., Fukuda H.;			
RT	"Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction method."			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB036341; BA88633.1; -			
DR	HSSP: P01607; 1REI.			
DR	INTERPRO: IPR003006; -			
DR	PFAM: PF00047; 1g; 2.			
Q9	SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;			

RESULT	5	
075725		
ID	075725	PRELIMINARY;
AC	075725;	PRT; 82 AA
DT	01-NOV-1998	(TREMBlrel. 08, Created)

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DT 01-NOV-1998 (TREMblrel. 08, last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE.
RA Fischer M., Kuepers R.;
RT "Human YH and Igm secreting intestinal plasma cells carry heavily
RT mutated YH region genes.";
RT Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
RL EMBL: AJ009522; CA080729.1; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF000047; Iq; 1.
FT NON_TER 1 82
FT NON_TER 82
FT Q0 SEQUENCE 82 AA; 9566 MW; 43253256570987A CRC64;

```

[illegible]

RESULT	6			
09UL84				
ID	09UL84	PRELIMINARY;	PRT;	122 AA.
AC	09UL84;			
DT	01-MAY-2000 (TREMBLrel, 13, Created)			
DT	01-MAY-2000 (TREMBLrel, 13, Last sequence update)			
DT	01-OCT-2000 (TREMBLrel, 15, Last annotation update)			
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).			
OS	Homo sapiens (human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98277139; PubMed=9614934;			
RA	Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,			
RA	Young D.C.;			
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal			
RT	fetus.";			
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).			
DR	EMBL; AF035030; AAD56266.1; -.			
DR	HSSP; P01772; ZF84.			
DR	INTERPRO; IPR003006; -.			
DR	PFAM; PF00047; 1g; 1.			
FT	NON_TER	1	1	
FT	NON_TER	122	122	
SO	SEQUENCE	122 AA;	13579 MW;	36054D41366545B8 CRC64;

```
Query Match      Score 314; DB 4; Length 122;  
Best Local Similarity   51.6%; Pred. No. 9.3e-25;  
Matches    63; Conservative     19; Mismatches    38; Indels       2; Gaps        2.  
  
0Y      20 OVOLOOGAGLIKPESETLSTLCAYGSGFSGYWMIROPFGKGLIEWTIGELINHSSTN-Y-78  
db      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
1 EVLLVESGGGVQPPSRSLRTLSGAASRFFSSNGGMHWRAOPDKGLEMAVALINDSDSNKKY 60
```

Oy	79	NPSLKSRYTISVDTRSKNOFSLKSSYAADPAAVYYCCAREIAR-PHREFDWMGGTLVT	137
	: :	: :	
Dd	61	ADSVAGRTITRDNSKNMMDLOMSLREDIAVYYCAKDENGRLVGTFPFDMGCGTLVT	120
Oy	138	SS	139
Dd	121	SS	122

RESULT	7		
Q9UL96			
ID	Q9UL96	PRELIMINARY;	PRT; 121 AA.
AC	Q9UL96;		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2000 (TREMBLrel. 14, last annotation update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT)		
OS	Homo sapiens (Human)		
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; Pubmed=9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RA	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal		
RT	fetus.";		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL; AF035018; AAD56254.1; -		
DR	INFERPRO; ipr003006; -		
DR	PFAM; PF00047; 19; 1. -		
FT	NON_TER 1		
FT	NON_TER 1		
FT	NON_TER 121		
Q0	SEQUENCE 121 AA; 13695 MW; D582D450596BD35 CRC64;		

[illegible]

RESULT	8	
O9QXF0		
ID	O9QXF0	PRELIMINARY; PRT: 117 AA.
AC	O9QXF0;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)	
DE	IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT)	
OS	Mus musculus (Mouse)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Clemons A., Rademakers A., Specht C., Koelsch E.,	
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBD databases.	
DR	EMBL; AJ225171; CAB65236.1; -	
DR	INTERPRO; IPR003006; -	
DR	PFAM; PF00047; 1q; 1.	

FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 13060 MW: D816AD0858A47EAC CRC64;

Query Match
Best Local Similarity 41.8%; Score 312.5; DB 11; Length 117;
Matches 58; Conservative 26; Mismatches 32; Indels 5; Gaps 2;

OY 20 QVQLDQWAGLLKPSSETLSLTCAVYGGSGFYWSMIRPPGKLEWIGELIN-HSGSTNY 78
Db 1 EVQLDQSGELVKGPGASVYMSCKASGYFTDYMMKWKSHGKSLKLEWIGDIPNNNGTSY 60
OY 79 NPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAYVYCAREIARPHRYF-DYWGCGTLVT 138
Db 61 NQKFKGKATLVYDKSSSTAYMQLNSLTSEDSAVYYCARD----KDYFPYWGCGTTLVTS 116
OY 139 S 139
Db 117 S 117

RESULT 9
OY 075739 PRELIMINARY; PRT; 78 AA.
AC 075739;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA Fischer M., Kuipers R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ009538; CAA08743.1;
DR INTERPRO: IPR003006;
DR PFM: PF00047; 1g.1.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA: 9031 MW: 2EB52A6C7A488066 CRC64;

Query Match
Best Local Similarity 41.7%; Score 312; DB 4; Length 78;
Matches 58; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 52 YMSWIRPPGKLEWIGELINHSSTNYNPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAY 111
Db 1 YMSWIRPPGKLEWIGELINHSSTNYNPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAY 60
OY 112 YVCARHSSWPIYFDNW 129
Db 61 YVCARHSSWPIYFDNW 78

RESULT 10
OY 090X9 PRELIMINARY; PRT; 117 AA.
AC 090X9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademakers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ225174; CAB65237.1;
DR INTERPRO: IPR003006;
DR PFM: PF00047; 1g.1.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 13000 MW: CDE2AF84D499734 CRC64;

Query Match
Best Local Similarity 41.2%; Score 308.5; DB 11; Length 117;
Matches 59; Conservative 26; Mismatches 29; Indels 9; Gaps 3;

OY 20 QVQLDQWAGLLKPSSETLSLTCAVYGGSGFYWSMIRPPGKLEWIGELIN-HSGSTNY 78
Db 1 EVQLDQSGELVKGPGASVYMSCKASGYFTDYMMKWKSHGKSLKLEWIGDIPNNNGTSY 60
OY 79 NPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAYVYCAREIARPHRYF-DYWGCGTLVT 136
Db 61 NQKFKGKATLVYDKSSSTAYMQLNSLTSEDSAVYYCARD-----RYAMDYWGCGTSTV 114
OY 137 VSS 139
Db 115 VSS 117

RESULT 11
OY 090L88 PRELIMINARY; PRT; 131 AA.
AC 090L88;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035026; AAD56262.1;
DR INTERPRO: IPR003006;
DR PFM: PF00047; 1g.1.
FT NON_TER 1 1
FT NON_TER 131 131
SQ SEQUENCE 131 AA: 14142 MW: 96E7D668E375DEAO CRC64;

Query Match
Best Local Similarity 41.2%; Score 308.5; DB 4; Length 131;
Matches 63; Conservative 20; Mismatches 37; Indels 11; Gaps 2;

OY 20 QVQLDQWAGLLKPSSETLSLTCAVYGGSGFYWSMIRPPGKLEWIGELIN-HSGSTNY 76
Db 1 EVQLDQSGELVKGPGASVYMSCKASGYFTDYMMKWKSHGKSLKLEWIGDIPNNNGTSY 60
OY 77 NPSLKSRTVTSVDTSKNPSLKLSSVTAADTAAYVYCAREIARPHRYF-DYWGCGTLVT 128
Db 61 DVAAPVKGKLTISRSRNTLYLRNLSKTEDTAVYCTGTITLIVITTSKRTSEY 120
OY 129 WGCGTLVTVSS 139
Db 117 WGCGTLVTVSS 139

Db 121 WGGGTLVTVSS 131

RESULT 12

09UL90

AC 09UL90: PRELIMINARY: PRT: 113 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL: AF035024; AAD56260.1; -

DR INTERPRO: IPR003006; -

DR PFAM: PF00047; 19; 1.

FT NON_TER 1 1

FT NON_TER 113 113

SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 40.8%; Score 305.5; DB 4; Length 113;

Best Local Similarity 50.4%; Pred. No. 6.2e-24;

Matches 61; Conservative 20; Mismatches 31; Indels 9; Gaps 2;

QY 20 QVQLQWAGLGLPKPSETLTCAVYGSGFSGYWMSIRPPGKGLMIGELINSGSTN-Y 78

Db 1 EVQLVDSGGVVOGGSGLRSCASGFTFSYGMHWROAPGGLMVGAFIRYDGSNKYY 60

QY 79 NPSLKRVTISVDTSKNPSLKLSTVADTAVYVCARELAARPHRYFYWGCGTLVTVS 138

Db 61 ADSVKRFTISRDNKSNLYLQWNSLRADDTAVYCAKDI-----NYWGGTLVTVS 112

QY 139 S 139

Db 113 S 113

RESULT 13

09UL92

AC 09UL92: PRELIMINARY: PRT: 124 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL: AF035022; AAD56258.1; -

DR INTERPRO: IPR003006; -

DR PFAM: PF00047; 19; 1.

FT NON_TER 1 1

FT NON_TER 124 124

SQ SEQUENCE 124 AA; 13580 MW; 1BAACBD96ACD2A2 CRC64;

RESULT 14

09UL71

AC 09UL71: PRELIMINARY: PRT: 121 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR HSPF: P01772; 2F84.

DR INTERPRO: IPR003006; -

DR PFAM: PF00047; 19; 1.

FT NON_TER 1 1

FT NON_TER 121 121

SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 40.7%; Score 304.5; DB 4; Length 121;

Best Local Similarity 50.4%; Pred. No. 8.6e-24;

Matches 61; Conservative 19; Mismatches 40; Indels 1; Gaps 1;

QY 20 QVQLQWAGLGLPKPSETLTCAVYGSGFSGYWMSIRPPGKGLMIGELIN-HSGSTN-Y 78

Db 1 EVQLVDSGGVVOGGSGLRSCASGFTFSYGMHWROAPGGLMVGAFIRYDGSNKYY 60

QY 79 NPSLKRVTISVDTSKNPSLKLSTVADTAVYVCARELAARPHRYFYWGCGTLVTVS 138

Db 61 ADSVKRFTISRDNKSNLYLQWNSLRADDTAVYCAKAKGVTTITDPRDWMGGTLVTVS 120

QY 139 S 139

Db 121 S 121

RESULT 15

09Y509

AC 09Y509: PRELIMINARY: PRT: 147 AA.

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98277139; PubMed=9614934;

RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,

RT "Myosin-reactive autoantibodies in rheumatic carditis and normal

RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR HSPF: P01772; 2F84.

DR INTERPRO: IPR003006; -

DR PFAM: PF00047; 19; 1.

FT NON_TER 1 1

FT NON_TER 121 121

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:43:34 ; Search time 26.57 Seconds
(without alignments)
150.571 Million cell updates/sec

Title: US-09-203-768a-4
Perfect score: 615
Sequence: 1 LMLPDTTGEIVMTQSPATLS.....QYNMPPYTFGGQTKLEIKR 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues
Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*

1: /SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseqp/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseqp/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseqp/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseqp/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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11: /SIDSI/gcgdata/geneseq/geneseqp/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqp/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseqp/AA1992.DAT:*
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19: /SIDSI/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseqp/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538.5	87.6	234	15	R52951 Human anti-IgE MAb
2	528.5	85.9	213	20	Y14207 HIV-1 gp120 peptid
3	528.5	85.9	213	20	Y14211 HIV gp120 protein
4	525	85.4	128	21	Y56720 Amino acid sequenc
5	523	85.0	129	14	R38672 VK325-JR2. Homo s
6	518	84.2	117	19	R47582 Human monoclonal a
7	513.5	83.5	349	12	R12128 IBI IgG aberrant 1
8	513.5	83.5	414	12	R13111 IBI IgG aberrant 1
9	513.5	83.5	414	12	R13018 IBI IgG aberrant 1
10	510.5	83.0	234	21	Y92239 Human bone marrow-
11	509.5	82.8	214	20	Y06842 Seg ID No:10 of JP
12	504.5	82.0	134	17	W11155 Anti-lung tumour a

13	499	81.1	129	14	R41286
14	497	80.8	129	14	R38673
15	494	80.3	150	19	W40069 Human monoclonal a
16	493.5	80.2	401	12	R12129 ORF 1 of IgG light
17	490.5	79.8	127	18	W08946 kappa light chain
18	489	79.5	109	20	Y08230 Human SCFV light c
19	489	79.5	115	14	R38648 Human V-kappa frag
20	489	79.5	115	15	R62928 Human V-kappa vk65
21	489	79.5	115	18	W41144 Human vkappa65.3 f
22	489	79.5	115	19	W62182 Human DNA vkappa65
23	482.5	78.5	214	20	Y08599 Anti-human TNF- α p
24	480	78.0	124	18	W24539 Immunoglobulin r10
25	476.5	77.5	120	17	W03946 DNA fragment vk65.
26	475.5	77.3	127	15	R50192 Light chain variab
27	475.5	77.3	127	20	Y26982 Light chain variab
28	474.5	77.2	109	20	W84096 Human V kappa subg
29	474	77.1	110	18	W27545 Human Ab light cha
30	474	77.1	115	20	Y40429 Y40429
31	469.5	76.3	127	15	R50187 Light chain variab
32	469.5	76.3	127	20	Y26980 Light chain variab
33	469.5	76.3	127	21	Y32407 Anti-P. aeruginosa
34	469.5	76.3	128	10	P91001 Light chain variab
35	466.5	75.9	127	15	R50191 Light chain variab
36	466.5	75.9	127	20	Y26981 Light chain variab
37	465	75.6	115	14	R38649 Human V-kappa frag
38	465	75.6	115	15	R62929 Human V-kappa vk65
39	465	75.6	115	17	W03947 DNA fragment vk65.
40	465	75.6	115	18	W41145 Human vkappa65.5 f
41	465	75.6	115	19	W62183 Human DNA vkappa65
42	465	75.6	115	20	Y40430 Amino acid sequenc
43	463.5	75.4	116	14	R38650 Human V-kappa frag
44	463.5	75.4	116	15	R62930 Human V-kappa vk65
45	463.5	75.4	116	17	W03948 DNA fragment vk65.

ALIGNMENTS

RESULT 1	
ID R52951	standard; Protein; 234 AA.
XX AC R52951:	
XX DT 27-OCT-1994	(first entry)
XX DE Human anti-IgE MAb light chain.	
XX KW Human IgE; CH4 region; triggers mediator release;	
XX KW Mast cells; Monoclonal antibody; allergy.	
XX OS Homo sapiens.	
XX FH Key	Location/Qualifiers
XX FT Region	21..128
XX FT	/label= light chain variable region
XX PN EP592230-A.	
XX PD 13-APR-1994.	
XX PF 07-OCT-1993;	93EP-0308006.
XX PR 07-OCT-1992;	92JP-0293800.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.	
XX PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;	
XX PI Yoshida T;	
XX DR WPI; 1994-120330/15.	
XX DR N-PSDB; 071872.	

F105 rearranged va
F105VK-F105JK. Ho
Human monoclonal a
ORF 1 of IgG light
kappa light chain
Human SCFV light c
Human V-kappa frag
Human V-kappa vk65
Human vkappa65.3 f
Human DNA vkappa65
Anti-human TNF- α p
Immunoglobulin r10
DNA fragment vk65.
Light chain variab
Light chain variab
Human V kappa subg
Human Ab light cha
Amino acid sequenc
Light chain variab
Light chain variab
Mouse anti-*Yersinia*
Anti-P. aeruginosa
Light chain variab
Light chain variab
Human V-kappa frag
Human V-kappa vk65
DNA fragment vk65.
Human vkappa65.5 f
Human DNA vkappa65
Amino acid sequenc
Human V-kappa frag
Human V-kappa vk65
DNA fragment vk65.

PT Human monoclonal anti-19E peptide antibody - inhibits histamine
 PT release from mast cells by allergen stimulation, useful for
 PT preventing allergies
 XX
 XX Claim 3, Page 12, 21pp; English.
 PS
 CC R52951 shows the light chain of a human type anti-19E peptide
 CC monoclonal antibody which inhibits the signal transmission for
 CC the release of chemical mediator from mast cells and basophils
 CC stimulated with allergen. The antibody can be used for the
 CC prophylaxis and the therapy of allergy.
 CC
 XX Sequence 234 AA:
 SQ

Query Match 87.6%; Score 538.5; DB 15; Length 234;
 Best Local Similarity 87.9%; Pred. No. 1.6e-32;
 Matches 102; Conservative 9; Mismatches 4; Indels 1; Gaps 1;

OY 1 LMLPTGTGIVMTOSPATLVSFGERATLSCRASOSVSSNLAWYOOKPGQAPRLILYGAS 60
 DB 13 Lwlpdtgeivmtqspatlsvsfgeratlsctrasqsvsnlamiyqkpkpqpaprlillygas 72

OY 61 TRATGIPARFSGSGSTFEPLTITSSLOSEDFAVYYCOQYNNMPYFGGCTLEIKR 116
 DB 73 tratiqparfsgsgstfcltisslqsedfalyccqysw-rtfifgqtkvdlk 127

RESULT 2
 ID Y14207 standard; peptide: 213 AA.
 AC Y14207;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE HIV-1 gp120 peptide.
 XX
 KM HIV, gp120; inhibitor; glycoprotein; CD4; leukocyte; infection.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9924065-A1.
 XX
 PD 20-MAY-1999.
 XX
 PE 10-NOV-1998; 98WO-US23905.
 XX
 PR 18-JUN-1998; 98US-0100764.
 PR 10-NOV-1997; 97US-0967708.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Hendrickson WA, Kwong PD, Samanen JM, Sodroski JG;
 PI Wyatt RT;
 XX
 DR WPI: 1999-337640/28.
 XX
 PT Inhibiting interaction between human immune deficiency virus gp120
 PT and CD4
 XX
 PS Disclosure: Fig 20; 41pp; English.
 XX
 CC This sequence represents a region of the HIV-1 gp120 protein.
 CC The invention relates to a method of inhibiting the interaction between
 CC human immune deficiency virus (HIV) glycoprotein gp120 and CD4 on
 CC leukocytes by administering an agent (I) containing functional groups
 CC that interact with gp120 to disrupt at least two specified interactions.
 CC (I) are used to treat and prevent infection by HIV.
 CC
 XX Sequence 213 AA:
 SQ

Query Match 85.9%; Score 528.5; DB 20; Length 213;
 Best Local Similarity 91.8%; Pred. No. 7.8e-32;
 Matches 101; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

OY 9 EIVMTQSPATLVSFGERATLSCRASOSVSSNLAWYOOKPGQAPRLILYGASTRATGIPA 68
 DB 1 elvltqspatlsvsfgeratlsctrasqsvsnlamiyqkpkpqpaprlillygastratgypa 60

OY 69 RFSGSGSTFEPLTITSSLOSEDFAVYYCOQYNNMPYFGGCTLEIKR 117
 DB 61 rfsgsgsgstfcltisslqsedfavyccqynmprryrtfifgqtkvdlk 110

RESULT 3
 ID Y14211 standard; peptide: 213 AA.
 AC Y14211;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE HIV gp120 protein fragment.
 XX
 KM HIV, gp120; glycoprotein; X-ray diffraction crystal; drug design;
 KM infection; therapy.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9924553-A2.
 XX
 PD 20-MAY-1999.
 XX
 PE 10-NOV-1998; 98WO-US23905.
 XX
 PR 18-JUN-1998; 98US-0100763.
 PR 10-NOV-1997; 97US-0966932.
 PR 10-NOV-1997; 97US-0966987.
 PR 10-NOV-1997; 97US-0967148.
 PR 10-NOV-1997; 97US-0967403.
 PR 24-NOV-1997; 97US-0976741.
 PR 18-JUN-1998; 98US-0100521.
 PR 18-JUN-1998; 98US-0100529.
 PR 18-JUN-1998; 98US-0100631.
 PR 18-JUN-1998; 98US-0100762.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Hendrickson WA, Kwong PD, Sodroski JG, Wyatt RT;
 PI WPI: 1999-337709/28.
 XX
 DR Crystals of human immune deficiency virus gp120 glycoprotein
 DR
 XX
 PT Disclosure: Fig 53; 41pp; English.
 PS
 CC This sequence represents a HIV gp120 glycoprotein fragment.
 CC The invention relates to crystals (A) for X-ray diffraction analysis
 CC comprise a polypeptide (I) representing part of the human immune
 CC deficiency virus (HIV) glycoprotein gp120. (A) are used to generate
 CC atomic coordinates for rational drug design, i.e. identification or
 CC design of agents that bind gp120, potentially useful for treating or
 CC preventing HIV infection. Variants of gp120 having a hidden, conserved
 CC neutralising epitope are useful in vaccines and to generate anti-HIV
 CC antibodies.
 CC
 XX Sequence 213 AA:
 SQ

Query Match 85.9%; Score 528.5; DB 20; Length 213;
 Best Local Similarity 91.8%; Pred. No. 7.8e-32;

Query Match 85.0%; Score 523; DB 14; Length 129;
 Best Local Similarity 87.3%; Pred. No. 1.2e-31;
 Matches 103; Conservative 7; Mismatches 6; Indels 2; Gaps 2;

OY 1 LMLPDTGEIVMTQSPAILSVSGGERATLSCRASQSVSSN-LAWYQKPGQAPRLLIYGA 59
 DB 13 LWLPTGELVITLSPGTLISPGERATLSCRASQSVSSYLAWYQKPGQAPRLLIYGA 72
 OY 60 SRRATGIPARFSGSGCTFEFTLTISLQSEDPFAVYCCOQYNNMPYTFEGGTRKLEIKR 117
 DB 73 SSRATGIPARFSGSGCTFEFTLTISLQSEDPFAVYCCOQYNNMPYTFEGGTRKLEIKR 129

RESULT 6
 W47582
 ID W47582 standard; Protein: 117 AA.
 AC W47582;
 DE 22-JUN-1998 (first entry)

XX Human monoclonal antibody light chain variable region.
 DE Human monoclonal antibody; hybridoma cell strain TTG6; hMab;
 KW antitetanus toxin.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Region 24..34
 FT /Label= CDR1
 FT Region 49..55
 FT /Label= CDR2
 FT Region 89..98
 FT /Label= CDR3

PN JPI0014570-A.
 PD 20-JAN-1998.
 XX 05-JUL-1996; 96JP-0194095.
 XX 05-JUL-1996; 96JP-0194095.
 PA (MATSU) MATSUDA M.
 PA (MOMI) MORINAGA & CO LTD.
 DR MPI; 1998-138233/13.
 DR N-PSDB; V18674.

PT New cDNA encoding human monoclonal antibody - useful for production
 PT of antibody by hybridoma techniques commercially
 PS Claim 4; Fig 2; 8pp; Japanese.

XX The present sequence represents a human monoclonal antibody (hMab)
 CC light chain variable region. The cDNA encoding the hMab can be used
 CC for commercial production of the hMab. The cDNA was isolated from an
 CC antitetanus toxin human monoclonal antibody producing hybridoma cell
 CC strain TTG6.
 XX Sequence 117 AA;

Query Match 84.2%; Score 518; DB 19; Length 117;
 Best Local Similarity 90.8%; Pred. No. 2.6e-31;
 Matches 99; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 9 EIVMTQSPATLISVSGGERATLSCRASQSVSSN-LAWYQKPGQAPRLLIYGA STRATGIPA 68
 DB 1 DIVMTGSPATLISVSGGERATLSCRASQSVSSN-LAWYQKPGQAPRLLIYGA STRATGIAA 60

OY 69 RFGSGSGCTFEFTLTISLQSEDPFAVYCCOQYNNMPYTFEGGTRKLEIKR 117
 DB 61 RFGSGSGCTFEFTLTISLQSEDPFAVYCCOQYNNMPYTFEGGTRKLEIKR 109

RESULT 7
 R12128
 ID R12128 standard; Protein: 349 AA.
 AC R12128;
 DE 01-AUG-1991 (first entry)

XX 1B1 IgG aberrant light chain with duplicated variable region.
 DE Immunoglobulin G; light chain; variable region; duplication;
 KW passive immunity; group B streptococci.
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..17
 FT /Label= leader peptide
 FT Region 18..130
 FT /Label= variable region
 FT /note= "L'V 1"
 FT Region 131..243
 FT /Label= variable region
 FT /note= "L'V 2"
 FT Region 244..345
 FT /Label= constant region

PN W09106305-A.
 PD 16-MAY-1991.
 XX 06-NOV-1990; 90MO-US06426.
 XX 07-NOV-1989; 89US-0432700.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 PA Shuford WW, Harris LJ, Raff HV;

DR MPI; 1991-163947/22.
 DR N-PSDB; Q11878.

PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class

PS Example 5; Fig 16; 104pp; English.

XX This sequence is deduced from the cDNA clone 4B9-VK15 and includes
 CC the amino acid sequence beyond the first stop codon. The clone is
 CC incomplete, starting from the G of the ATG initiator codon, but the
 CC initial Met is given. Antibody molecules of the invention can
 CC include one or two aberrant light chains containing a duplicated
 CC variable region, to produce heavier antibodies. These heavier
 CC antibodies were found to have higher avidity than antibodies with
 CC just a single copy of the L'V region. The antibodies can be used to
 CC treat disease, e.g. infection by Streptococcus agalactiae. They are
 CC able to pass across the placenta.
 CC See also Q11879 and Q11880.

XX Sequence 349 AA;

Query Match 83.5%; Score 513.5; DB 12; Length 349;
 Best Local Similarity 85.5%; Pred. No. 1.5e-30;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

XX Sequence 414 AA:
SQ

Query Match 83.5%; Score 513.5; DB 12; Length 414;
Best Local Similarity 85.5%; Pred. No. 1.8e-30;
Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDPTEIVMTOSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGCAPRLIYGAS 60
DB 13 LWPDPTEIVMTOSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGCAPRLIYGAS 72
OY 61 TRATGIPARFSGSGTEFTLTSSLSQSDFAVYCYQOYNNMWP-YTFGQTKLEIK 116
DB 73 nratgiparfsgsgtdftltsslsqsdFAVYCYQOYNNMWPYTFGQTKLEIK 129

RESULT 10
Y92239
ID Y92239 standard; Protein: 234 AA.

AC Y92239;
XX
XX 10-AUG-2000 (first entry)
XX
XX Human bone marrow-derived serum protein 1.
XX
XX Bone marrow-derived serum protein; immunoglobulin kappa light chain;
XX BMDSP-1; cytoskeletal; anti-HIV; antileishmanic; antitubercular;
XX anti-inflammatory; antitachytic; antisclerotic; hypotensive; antiviral;
XX antiparasitic.

OS Homo sapiens.
XX

Key Location/Qualifiers
FT 18 /note= "potential casein kinase II phosphorylation site"
FT Modified-site
FT 34 /note= "potential casein kinase II phosphorylation site"
FT Domain
FT 36..110 /label= "immunoglobulin_domain"
FT 42 /note= "potential protein kinase C phosphorylation site"
FT Modified-site
FT 72 /note= "potential protein kinase C phosphorylation site"
FT Modified-site
FT 87 /note= "potential casein kinase II phosphorylation site"
FT Modified-site
FT 96 /note= "potential casein kinase II phosphorylation site"
FT Modified-site
FT 122 /note= "potential casein kinase II phosphorylation site"
FT Domain
FT 147..216 /label= "immunoglobulin_domain"
FT Domain
FT 151..173 /label= "immunoglobulin"
FT /label= "signature_sequence"
FT /note= "immunoglobulin"
FT Modified-site
FT 182 /note= "potential casein kinase II phosphorylation site"
FT Modified-site
FT 184 /note= "potential casein kinase II phosphorylation site"
FT Domain
FT 190..233 /label= "signature_sequence"
FT /label= "immunoglobulin"
FT /note= "immunoglobulin"
FT Modified-site
FT 202 /note= "potential casein kinase II phosphorylation site"
FT Domain
FT 212..229 /label= "signature_sequence"
FT /note= "immunoglobulin"

XX WO200020586-A2.
XX 13-APR-2000.
XX PD
XX

PF 01-OCT-1999; 99WO-US222908.
XX
XX 02-OCT-1998; 98US-0165621.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Tang YT, Corley NC, Guegler KJ, Lu DAM;
XX
XX

DR WPI: 2000-303775/26.
XX
XX N-PSDB: A09154.
XX

PT Purified polypeptide for treating or preventing disorders associated
PT with decreased expression or activity of bone marrow-derived serum
PT proteins
XX

PS Claim 1: Page 68-69; 72pp; English.

XX Human bone marrow-derived serum proteins (BMDSP) 1 has chemical and
XX structural similarity with immunoglobulin kappa light chain. BMDSP-1
XX and BMDSP-2 are useful for treating or preventing a disorder associated
XX with decreased expression or activity of BMDSP.
XX Antagonists of BMDSP are useful for treating or preventing a disorder
XX associated with increased expression or activity of bone marrow-derived
XX serum proteins. The disorders include cancers (melanoma, adenocarcinoma,
XX sarcoma), immune disorders (acquired immunodeficiency syndrome (AIDS),
XX asthma, atherosclerosis, Crohn's disease, bronchitis, multiple sclerosis,
XX osteo- and rheumatoid arthritis), viral infections, parasitic infections
XX (schistosoma, tapeworm), and vascular disorders (arteriosclerosis,
XX hypertension, vasculitis).

SQ Sequence 234 AA:

Query Match 83.0%; Score 510.5; DB 21; Length 234;
Best Local Similarity 85.5%; Pred. No. 1.7e-30;
Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDPTEIVMTOSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGCAPRLIYGAS 60
DB 13 LWPDPTEIVMTOSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGCAPRLIYGAS 72
OY 61 TRATGIPARFSGSGTEFTLTSSLSQSDFAVYCYQOYNNMWPYTFGQTKLEIK 117
DB 73 nratgiparfsgsgtdftltsslsqsdFAVYCYQOYNNMWPYTFGQTKLEIK 128

RESULT 11

ID Y06842
Y06842 standard; Protein: 214 AA.

AC Y06842;

XX 25-JUN-1999 (first entry)

XX Seq ID No.10 of JPI1089576.

XX AntiHBS; monoclonal antibody; Epstein Barr virus; EBV; adr type;
XX human; HBS antigen; hepatitis C.

XX Homo sapiens.

XX JPI1089576-A.

XX 06-APR-1999.

XX 19-SEP-1997; 97JP-0255705.

XX 19-SEP-1997; 97JP-0255705.

XX (NISN) NISSHINBO IND INC.

XX WPI: 1999-281053/24.

XX N-PSDB: X32826.
XX DR

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XX Anti-HBs monoclonal antibody - produced without the risk of Epstein
PT Barr virus contamination
XX
XX Disclosure: Page 9-10; 12pp; Japanese.
XX
CC The invention relates to an anti-HBs monoclonal antibody having the
CC following properties: (A) CDR-3 of H chain variable region; (B) it
CC contains no Epstein Barr virus (EBV); (C) it binds at least one adr type
CC among human HBs antigens. The anti-HBs monoclonal antibody is high in
CC antibody titer and has low risk of EBV contamination. It can be used to
CC prevent hepatitis C.
XX
SQ Sequence 214 AA:

Query Match 82.8%; Score 509.5; DB 20; Length 214;
Best Local Similarity 93.6%; Pred. No. 1.9e-30;
Matches 102; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGQAPRLLIYGASTRATGIPA 68
DB 1 elvmtqspatlsvspgeratlscrasqsvrnlawyqkpgqaprllyaastratgipa 60
QY 69 RFGSGSGSEFTLTLSLQSEDFAVYYCCQYNNMPYTFGQGTLEIKR 117
DB 61 rfgsgsgseftltlsslqsedfavyycqygnw-frtfggtkveikr 108

RESULT 12
W1155
ID W1155 standard; Protein; 134 AA.
XX
XX W1155;
AC
XX
XX 14-MAY-1997 (first entry)
DE
XX Anti-lung tumour antigen monoclonal antibody light chain.
XX
XX Light chain monoclonal; antibody; TB2A36C3; lung; tumour; EBV;
XX Epstein-Barr virus; TB945; human; B cell; screen; antigen;
XX carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;
XX cell.
XX
XX Homo sapiens.
XX OS
XX MO9628473-A1.
XX PN
XX 19-SEP-1996.
XX PD
XX 18-MAR-1996; 96WO-US03661.
XX PF
XX 16-MAR-1995; 95US-0405034.
XX PR
XX (MEDE/) MEDENICA R D.
XX PA
XX Mukerjee S;
XX PI
XX WPI: 1996-433764/43.
XX DR
XX N-PSDB: T33664.
XX
XX Anti-lung tumour antigen monoclonal antibody TB2A36C3 - produced by
XX Epstein-Barr virus transformation of human lung cancer patient
XX B-cells, useful in conjunction with other agents for lysis of
XX tumours
XX
XX Claim 12; Page 25; 46pp; English.
XX
XX The present sequence is the light chain from the monoclonal
XX antibody (MAB) TB2A36C3, which has high specificity against lung
XX tumour antigens and is produced by an Epstein-Barr virus (EBV)
XX transformed T9945 human B cell line. The MAB can be used to screen
XX serum or tissue samples for a carcinoma associated antigen, lyse

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CC tumours in anti-tumour therapy (optionally with other agents) and
CC activate immune competent CD4 or CD8 cells in a patient's blood
CC system.
CC Tumour draining lymph nodes obtained from a non-SCIC (small cell
CC lung cancer) patient were cut into fine pieces and washed. Pure B
CC cells, isolated using CD19 coated immunomagnetic beads, were
CC immortalised by EBV transformation, and plated and assayed for
CC activity. Clones which showed positive reactivity with autologous
CC tumour cells from the patient and the SCIC cell line NCIM69, were
CC subjected to limiting dilution to prepare the MAb.
XX
SQ Sequence 134 AA:

Query Match 82.0%; Score 504.5; DB 17; Length 134;
Best Local Similarity 84.7%; Pred. No. 2.8e-30;
Matches 100; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 LMLPDTGIEIVMTQSPATLSVSPGERATLSCRASQSV-SNLAWYQKPGQAPRLLIYGA 59
DB 13 lmlpdtgeivltqspatlsvspgeratlscrasqsfrrslawyqkpgqapsllyga 72
QY 60 SRRATGIPARFSGSGSEFTLTLSLQSEDFAVYYCCQYNNMPYTFGQGTLEIKR 117
DB 73 stratgipdrfsgsgseftltlsslqsedfavyycqygsaarylfggtkveikr 130

RESULT 13
R41286
ID R41286 standard; Protein; 129 AA.
XX
XX R41286;
AC
XX
XX 01-NOV-1993 (first entry)
DE
XX F105 rearranged variable region light chain.
XX
XX Monoclonal antibody; MAB; envelope; glycoprotein; gp120; HIV; AIDS;
XX CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
XX chain; epitope; immune deficiency.
XX
XX Homo sapiens.
XX OS
XX FH
XX Key Location/Qualifiers
XX Peptide 1..19
XX FT /label= sig_peptide
XX FT 20..129
XX FT /label= mat_protein
XX PN
XX MO9312232-A.
XX PD
XX 24-JUN-1993.
XX PF
XX 10-DEC-1992; 92WO-US10928.
XX PR
XX 10-DEC-1991; 91US-0804652.
XX PA
XX (DAND ) DANA FARBER CANCER INST INC.
XX PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.
XX PI
XX Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
XX WPI: 1993-214174/26.
XX DR
XX N-PSDB: Q49155.
XX
XX DNA segments encoding monoclonal antibody - which binds to gp120
XX and neutralises HIV, for treating AIDS, and for diagnosing and
XX monitoring HIV infection
XX
XX Claim 10; Page 79; 109pp; English.
XX
XX mRNA from the known hybridoma F105 was converted to cDNA and this
XX subjected to PCR amplification using primers corresp. to appropriate

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CC parts of the heavy or light chains and having restriction sites to permit cloning. The extension prods. were isolated and sequenced.
 CC The recombinant human monoclonal antibody (MAb) binds to a
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad
 CC range of HIV isolates. The MAb may be used to treat immune
 CC deficiency, esp. at doses of 0.1-10 mg/Kg.

Sequence 129 AA:

Query Match 81.1%; Score 499; DB 14; Length 129;
 Best Local Similarity 84.7%; Pred. No. 6, 8e-30;
 Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 2;

OY 1 LMLPPTGELVMTQSPATLSVSPGERATLSCRASQSVSN-LAWYQOKPGQAPRLIYGA 59
 |||
 Db 13 lwpdttgclvtlqspgtlslsageratlscrasgsvsrslawyqkpgqaprlillyga 72
 OY 60 STRATGIPARFSGSGGTEFTLTISLSQSEDFAVYVYCOQYNNMPPYTFGQTKLEIKR 117
 |||
 Db 73 sratgipdrfsgsggtfdltlstrvpedfavyycqgdn-svctfsgtklelkr 129

RESULT 14

R38673 R38673 standard; Protein; 129 AA.

AC R38673;

DT 01-NOV-1993 (first entry)

DE F105VK-F105JK.

KM Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;
 KM CD4 receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
 KM chain; epitope; immune deficiency.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /label= sig_peptide
 FT 21..129
 FT Protein /label= mat_protein
 FT 1..116
 FT Region /label= F105VK
 FT 117..129
 FT /label= F105JK
 FT 44..55
 FT Region /label= CDR1
 FT 71..77
 FT Region /label= CDR2
 FT 110..117
 FT /label= CDR3
 FT Misc-difference 1
 FT /note= "Met encoded by ATC (sic)"
 FT Misc-difference 35
 FT /note= "Pro encoded by GCA (sic)"
 FT Misc-difference 99
 FT /note= "Leu encoded by GTG (sic)"
 FT Misc-difference 113
 FT /note= "Gly encoded by GAT (sic)"
 FT Misc-difference 114
 FT /note= "Ser encoded by AAC (sic)"
 FT Misc-difference 116
 FT /note= "Pro encoded by GTT (sic)"

PN MO9312232-A.

PD 24-JUN-1993.

PF 10-DEC-1992; 92WO-US10928.

XX 10-DEC-1991; 91US-0804652.

XX (DAND) DANA FARMER CANCER INST INC.

PA (NEW-) NEW ENGLAND DEACONNESS HOSPITAL CORP.

PI Haseltine WA, Marasco WA, Posner MR, Sodroski JG;

DR WPI: 1993-214174/26.

DR N-PSDB; Q42706.

PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection

PS Disclosure; Page 74-75; 109pp; English.

CC The nucleotide sequence of F105 VK (Q42707 - sequence differs from
 CC other F105 VK sequences given elsewhere in the specification) was
 CC compared with germline gene HumvK325 (Q42706), showing 97.7%
 CC similarity. By nucleotide sequence analysis, F105 appears to
 CC be derived from a member of the VK III subgroup gene family.

XX Sequence 129 AA:

Query Match 80.8%; Score 497; DB 14; Length 129;
 Best Local Similarity 84.7%; Pred. No. 9, 5e-30;
 Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 2;

OY 1 LMLPPTGELVMTQSPATLSVSPGERATLSCRASQSVS-SNLAWYQOKPGQAPRLIYGA 59
 |||
 Db 13 lwpdttgclvtlqspgtlslsageratlscrasgsvsrslawyqkpgqaprlillyga 72

OY 60 STRATGIPARFSGSGGTEFTLTISLSQSEDFAVYVYCOQYNNMPPYTFGQTKLEIKR 117
 |||
 Db 73 sratgipdrfsgsggtfdltlstrvpedfavyycqgdn-svctfsgtklelkr 129

RESULT 15

W40069 W40069 standard; Protein; 150 AA.

AC W40069;

DT 29-MAY-1998 (first entry)

DE Human monoclonal antibody H11 protein variable region H chain.

XX H11, monoclonal antibody; MAb; C-antigen; variable region heavy chain;
 KW V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;
 KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
 KW malignant melanoma; adenocarcinoma; small cell lung carcinoma.

OS Homo sapiens.

PN WO9744461-A2.

PD 27-NOV-1997.

PF 22-MAY-1997; 97WO-US08962.

PR 22-MAY-1996; 96US-0657449.

PA (NOVO-) NOVOPHARM BIOTECH INC.

PI Dan MD, Kaplan HA, Maiti PK;

DR WPI: 1998-018515/02.

DR N-PSDB; V10111.

PT Antigen binding fragment from monoclonal antibody, H11 - allows
 PT tumour specific detection and treatment of neoplasia

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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:44:01 ; Search time 23.59 seconds
(without alignments)
336.769 Million cell updates/sec

Title: US-09-203-768a-4

Perfect score: 615

Sequence: 1 LMLPDTTGEIWMQSPATLS.....QYNNMPYTFGGQTKLEIKR 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	95.7	128	S40343	Ig kappa chain V-J
2	574.5	93.4	117	S40362	Ig kappa chain - h
3	562	91.4	131	S40328	Ig kappa chain - h
4	539.5	87.7	123	S40378	Ig kappa chain - h
5	530.5	86.3	128	A56701	Ig kappa chain V r
6	527	85.7	115	K3HUC1	Ig kappa chain pre
7	526.5	85.6	107	S34005	Ig kappa chain V r
8	526	85.5	115	A30553	Ig kappa chain pre
9	525.5	85.4	144	PI0106	Ig kappa chain pre
10	523	85.0	116	B26555	Ig kappa chain V-I
11	522	84.9	110	S40326	Ig kappa chain V-J
12	518.5	84.3	128	S40379	Ig kappa chain V-J
13	514	83.6	215	JEO244	Ig kappa chain NTG
14	513.5	83.5	129	S29627	Ig kappa chain V r
15	511.5	83.2	114	S40375	Ig kappa chain V-J
16	510	82.9	129	K3HUA	Ig kappa chain pre
17	510	82.9	129	S49532	Ig kappa chain V r
18	510	82.9	129	S46369	Ig kappa chain V r
19	510	82.9	134	S38643	Ig kappa chain V r
20	509.5	82.8	128	S40345	Ig kappa chain V-J
21	509	82.8	129	K3HUI	Ig kappa chain pre
22	505	82.1	108	S40377	Ig kappa chain - h
23	504	82.0	109	K3HUPM	Ig kappa chain V-I
24	502	81.6	129	A33274	Ig kappa chain pre
25	499	81.1	128	S20636	Ig kappa chain V r
26	498	81.0	130	S20637	Ig kappa chain V r
27	496	80.7	114	S54905	Ig kappa chain V r
28	496	80.7	130	S40360	Ig kappa chain - h
29	494	80.3	129	S40363	Ig kappa chain - h

30	493.5	80.2	128	1	K3HUA1	Ig kappa chain pre
31	492.5	80.1	131	2	S40346	Ig kappa chain V-J
32	490.5	79.8	111	2	S23628	Ig kappa chain V r
33	489.5	79.6	125	2	S40344	Ig kappa chain V-J
34	489	79.5	115	1	K3HUC	Ig kappa chain pre
35	485.5	78.9	129	2	S40325	Ig kappa chain - h
36	485	78.9	121	2	S40327	Ig kappa chain - h
37	484	78.7	124	2	S20633	Ig kappa chain - h
38	482.5	78.5	215	2	JEO243	Ig kappa chain NTG
39	479.5	78.0	119	2	S41816	Ig kappa chain V r
40	478	77.7	98	2	I30608	Ig kappa chain V-I
41	476	77.4	95	2	PH0868	Ig kappa chain V-I
42	475	77.2	109	2	H30601	Ig kappa chain V-I
43	471.5	76.7	108	2	G44151	Ig kappa chain V r
44	467	75.9	145	2	S20631	Ig kappa chain - h
45	465	75.6	108	2	C30608	Ig kappa chain V-I

ALIGNMENTS

RESULT 1
S40343
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #ext_change 21-Jan-2000
C:Accession: S40343
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40343
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-references: EMBL:X72453; NID:g441374; PIDN:CA51121.1; PID:g441375
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 95.7%; Score 588.5; DB 2; Length 128;
Best Local Similarity 97.4%; Pred. No. 5e-42;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 LMLPDTTGEIWMQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLTYGAS 60
Db 13 LMLPDTTGEIWMQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLTYGAS 72
QY 61 TRATGIPARFSGSGSTFEFTLTISLQSEDFAYVYCOQYNNMPYTFGGQTKLEIKR 117
Db 73 TRATGIPARFSGSGSTFEFTLTISLQSEDFAYVYCOQYNNMPYTFGGQTKLEIKR 128
RESULT 2
S40362
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #ext_change 21-Jan-2000
C:Accession: S40362
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40362
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <KLE>
A:Cross-references: EMBL:X72472; NID:g441412; PID:g441413
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 93.4%; Score 574.5; DB 2; Length 117;
 Best Local Similarity 96.6%; Pred. No. 6.6e-41;
 Matches 112; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
 |||||
 DB 3 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 62
 |||||
 OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 116
 |||||
 DB 63 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 117
 |||||

RESULT 3

S40328
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40328
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891
 A:Accession: S40328
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-131 <KLE>
 A:Cross-references: EMBL:X72438; NID:g441344; PIDN:CA51106.1; PID:g441345
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:35-109/Domain: Immunoglobulin homology <IMM>

Query Match 91.4%; Score 562; DB 2; Length 131;
 Best Local Similarity 89.7%; Pred. No. 7.9e-40;
 Matches 105; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
 |||||
 DB 12 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAY 71
 |||||
 OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 117
 |||||
 DB 72 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 128
 |||||

RESULT 4

S40378
 Ig kappa chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40378
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891
 A:Accession: S40378
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-123 <KLE>
 A:Cross-references: EMBL:X72488; NID:g441444; PIDN:CA51156.1; PID:g441445
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:29-103/Domain: Immunoglobulin homology <IMM>

Query Match 87.7%; Score 539.5; DB 2; Length 123;
 Best Local Similarity 87.3%; Pred. No. 5.3e-38;
 Matches 103; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
 |||||

DB 6 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 65
 OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 117
 |||||
 DB 66 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 123
 |||||

RESULT 5

A56701
 Ig kappa chain V region precursor (HuA) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
 C:Accession: A56701
 R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
 J. Biol. Chem. 270, 12457-12465, 1995
 A:Title: Human and mouse monoclonal antibodies to blood group A substance, which are
 A:Reference number: A56701; MUID:95279371
 A:Accession: A56701
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-128 <NIC>
 A:Cross-references: GB:I41174; NID:9762823; PIDN:AA64877.1; PID:9762824
 C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:36-110/Domain: Immunoglobulin homology <IMM>

Query Match 86.3%; Score 530.5; DB 2; Length 128;
 Best Local Similarity 88.0%; Pred. No. 3e-37;
 Matches 103; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

OY 1 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
 |||||
 DB 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQOKPGQAPRLIYDAS 72
 |||||
 OY 61 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 117
 |||||
 DB 73 TRATGIPARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTKEIKR 128
 |||||

RESULT 6

K3HUC1
 Ig kappa chain precursor V-II region (CLL) - human
 N:Alternate names: Rheumatoid factor
 C:Species: Homo sapiens (man)
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
 C:Accession: A01898
 R:Jirik, F.R.; Sorge, J.; Fong, S.; Heltmann, J.G.; Curo, J.G.; Chen, P.P.; Goldfien
 Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
 A:Title: Cloning and sequence determination of a human rheumatoid factor light-chain
 A:Reference number: A01898; MUID:86177570
 A:Accession: A01898
 A:Molecule type: DNA
 A:Residues: 1-115 <JIR>
 A:Note: The sequence was determined from the germline gene
 C:Genetics:
 A:Gene: GDB:IGKV3
 A:Cross-references: GDB:136266
 A:Map position: 2p12-2p11
 A:Introns: 17/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L) chain disulfide bonds. In some cases, such as IGA and IGH, the subunits associate into C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
 C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-115/Product: Rheumatoid factor, Ig kappa chain V-II region (CLL) #status predicted
 F:21-43/Region: framework 1
 F:36-110/Domain: Immunoglobulin homology <IMM>
 F:44-54/Region: complementarity-determining 1
 F:55-69/Region: framework 2
 F:70-76/Region: complementarity-determining 2
 F:77-108/Region: framework 3
 F:109-115/Region: complementarity-determining 3

F:43-108/Disulfide bonds: #status predicted

Query Match 85.7%; Score 527; DB 1; Length 115;
Best Local Similarity 97.1%; Pred. No. 5.3e-37;
Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LMLPDTTGEIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
|||||
DB 13 LMLPDTTGEIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 72
QY 61 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMP 103
|||||
DB 73 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMP 115

RESULT 7
S34005
Ig kappa chain V region - human

C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34005; S30524
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A:Reference number: S34001; MUID:93209281
A:Accession: S34005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <MAR>
A:Cross-references: EMBL:Z18330
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 526.5; DB 2; Length 107;
Best Local Similarity 96.3%; Pred. No. 5.5e-37;
Matches 104; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 EIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 68
|||||
DB 1 EIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
QY 69 RFGSGSGTEFTLTISLQSEDFAYVYCOQYNNMPYTGQGTKEIK 116
|||||
DB 61 RFGSGSGTEFTLTISLQSEDFAYVYCOQYNNMPYTGQGTKEIK 107

RESULT 8
A30553

Ig kappa chain precursor V-III region (Hab) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000
C:Accession: A30553
R:Liu, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson, D.
J. Immunol. 142, 688-694, 1989
A:Title: Characterization of four homologous L chain variable region genes that are rela
A:Reference number: A30553; MUID:89093959
A:Accession: A30553
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-115 <LIU>
A:Note: the sequence was determined from the differentiated gene
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 85.5%; Score 526; DB 2; Length 115;
Best Local Similarity 97.1%; Pred. No. 6.5e-37;
Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LMLPDTTGEIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
|||||
DB 13 LMLPDTTGEIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 72
QY 61 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMP 103
|||||
DB 73 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMP 115

RESULT 9
PL0106

Ig kappa chain precursor V-J-C region (LSI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma s
A:Reference number: PL0106; MUID:8923583
A:Accession: PL0106
A:Molecule type: mRNA
A:Residues: 1-144 <SIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>
F:36-110/Domain: immunoglobulin homology <IMM>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match 85.4%; Score 525.5; DB 2; Length 144;
Best Local Similarity 87.2%; Pred. No. 8.8e-37;
Matches 102; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

QY 1 LMLPDTTGEIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60
|||||
DB 13 LMLPDTTGEIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 72
QY 61 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMPYTGQGTKEIK 117
|||||
DB 73 TRATGIPARSSGSGTEFTLTISLQSEDFAYVYCOQYNNMPYTGQGTKEIK 128

RESULT 10
B26555

Ig kappa chain V-III region (Ger) - human
C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C:Accession: B26555
R:Midgaugh, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A:Title: Atycical glycosylation of an IgG monoclonal cryoimmunoglobulin.
A:Reference number: A92630; MUID:87137666
A:Accession: B26555
A:Molecule type: protein
A:Residues: 1-116 <MID>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.0%; Score 523; DB 2; Length 116;
Best Local Similarity 91.7%; Pred. No. 1.1e-36;
Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 9 EIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 68
|||||
DB 1 EIVMTQSPATISVSPGERATISCRASQSVSSNLAWYQOKPGQAPRLIYGAS 60

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chI) gene recombination
A:Reference number: S46369; MUID:94313975
A:Accession: S46375
A:Molecule type: mRNA
A:Residues: 1-114 <BEM>
A:Cross-references: EMBL:Z27176; NTD:8415967; PTDN:CAAB1700.1; PID:9415968
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:20-95/Domain: Immunoglobulin homology <1Im>

	Query Match	83.2%	Score	511.5	DB	2	Length	114	
	Best Local Similarity	86.8%	Pred.	No. 1e-35					
	Matches	99	Conservative	8	Mismatches	6	Indels	1	Gaps
Oy	5	DTTGELVMTOSPATLSVSPGERATISCRASOSVSSN-LAMWOOKPQOARLLIYGASTRA	63						
		: : : : : :							
Dd	1	DTTGEIVLTQSCTGTSLSFGERATISCRASOSISSLYLAMWOOKPQOARLLIYGASSRA	60						
Oy	64	TGIPARFSGSAGTEFTLTISSLOJEDFAVVYCOOYNMNPPTFGGTLEIKR	117						
		: : : : : :							
Dd	61	TGIPRFSGSAGCTDETLTISRLEDPEDRVYICOOYGSSPTTFGGGTLEIKR	114						

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Search completed: March 9, 2001, 16:44:01
Job time: 60 sec
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OY 61 TRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOQYNNMPYFGQTKLEIKR 117
 |||||||||||||||||||
 DB 73 TRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOQYNNMPYFGQTKLEIKR 129

RESULT 2

KV3L_HUMAN STANDARD; PRT; 129 AA.

AC P18135;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HAH PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE-88171307; PubMed-3127527;
 RA Kips T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.

DR PIR: P10022; K3HHA.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 DR Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JKL SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 82.9%; Score 510; DB 1; Length 129;
 Best Local Similarity 85.6%; Pred. No. 7.2e-43;
 Matches 101; Conservative 7; Mismatches 8; Indels 2; Gaps 2;

OY 1 LMLPTGTGIVMTQSPATISVSGERATLSCRAOSVSSN-LAWYQKQGAAPRLIYGA 59
 |||||||||||||||||||
 DB 13 LMLPTGTGIVMTQSPATISVSGERATLSCRAOSVSSN-LAWYQKQGAAPRLIYGA 72

OY 60 STRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOQYNNMPYFGQTKLEIKR 117
 |||||||||||||||||||
 DB 73 SSRATGIPDRFSSGSGTDFLTLSRLPEDPAYVYCCQYGI-SPRTFQGTKEIKR 129

RESULT 3

KV3M_HUMAN STANDARD; PRT; 129 AA.

AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION HIC PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.

RA MEDLINE-88171307; PubMed-3127527;

RA Kips T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RL J. Exp. Med. 167:840-852(1988).
 CC -I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
 CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC
 CC LEUKEMIA.

DR PIR: P10021; K3HHT.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 DR Immunoglobulin V region; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 56 70 FRAMEWORK 2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 78 109 FRAMEWORK 3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 119 129 JKL SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON_TER 129 129
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

Query Match 82.8%; Score 509; DB 1; Length 129;
 Best Local Similarity 84.7%; Pred. No. 9e-43;
 Matches 100; Conservative 9; Mismatches 7; Indels 2; Gaps 2;

OY 1 LMLPTGTGIVMTQSPATISVSGERATLSCRAOSVSSN-LAWYQKQGAAPRLIYGA 59
 |||||||||||||||||||
 DB 13 LMLPTGTGIVMTQSPATISVSGERATLSCRAOSVSSN-LAWYQKQGAAPRLIYGA 72

OY 60 STRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOQYNNMPYFGQTKLEIKR 117
 |||||||||||||||||||
 DB 73 SSRATGIPDRFSSGSGTDFLTLSRLPEDPAYVYCCQYGI-SPRTFQGTKEIKR 129

RESULT 4

KV3F_HUMAN STANDARD; PRT; 109 AA.

AC P01624;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION POM.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE.

RA Klapper D.G., Capra J.D.;
 RT "The amino acid sequence of the variable regions of the light chains
 RT from two idiootypically cross reactive IGM anti-gamma globulins.";
 RL Ann. Immunol. (Paris) 127C:261-271(1976).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.

DR PIR: A01897; K3HUPM.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -.
 DR PFAM: PF00047; 19; 1.
 DR Immunoglobulin V region.
 KW Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SQ SEQUENCE 109 AA; 11922 MW; 62821DDCA8ABA86 CRC64;

Query Match 82.0%; Score 504; DB 1; Length 109;
 Best Local Similarity 90.9%; Pred. No. 2.3e-42;
 Matches 100; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

```

OY 9 EIVMTQSPATLTSVSGERATLISCRASQSVS-SNLMAYOOKPGQAPRLIYGASTRATGIP 67
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1 EIVMTQSPVTLTSVSGERATLISCRASQSVSNLYLAWYOOKPGSGRRLIYGASTRATGIP 60
OY 68 ARFSGSGSGTEFTLTITSSLOSDFAVYVYCCQYNNMPPYFGGTRKLEIKR 117
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 61 ARFSGSGSGTEFTLTITSSLOSDFAVYVYCCQYNNMPP-FTGGGTRVEIKR 109
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
KV3K_HUMAN STANDARD: PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION IARC/BL41 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86041852; PubMed=2997711;
RX Klobbeck H.G., Melndi A., Combiatio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: Z00021; CAA77316.1; -.
DR PIR: A01899; K3HU41.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-II REGION IARC/BL41.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 118 128 JKI SEGMENT.
FT DISULFD 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 80.2%; Score 493.5; DB 1; Length 128;
Best Local Similarity 82.9%; Pred. No. 2.8e-41;
Matches 97; Conservative 7; Mismatches 12; Indels 1; Gaps 1.

OY 1 LMLPDTGEIYVMTQSPATLTSVSGERATLISCRASQSVSSNLMAYOOKPGQAPRLIYGAS 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 13 LMLPDTGEIYVMTQSPATLTSVSGERATLISCRASQSVSSNLMAYOOKRQSGRRLIYRDAS 72
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 61 TRANGIPARFSGSGSGTEFTLTITSSLOSDFAVYVYCCQYNNMPPYTFGGGTRKLEIKR 117
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 73 SRANGIPDRFSGSGSGTDTLTITSLRLEPDEFAVYVYCCQYST-SPTFGGTRKLEIKR 128
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
KV3I_HUMAN STANDARD: PRT; 115 AA.
AC P04433;

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CC
DR DR 13-AUG-1987 (Rel. 05, Created)
DT DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE DE 13-AUG-1987 (Rel. 05, Last annotation update)
DS DS 15-JUL-1989 (Rel. 38, Last annotation update)
OS OS IG KAPPA CHAIN V-IIII REGION VC PRECURSOR (FRAGMENT).
OC OC Homo sapiens (Human).
CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN RN Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RP RP [1]
RX RX SEQUENCE FROM N.A. PubMed=6440122;
RA RA MEDLINE=85087932;
RT RT Pech M., Zachau H.G.;
RL RL "Immunoglobulin genes of different subgroups are interdigitated
within the VK locus.";
CC CC Nucleic Acids Res. 12:9229-9236(1984).
-----
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CC CC or send an email to license@isb-sdb.ch).
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DR DR EMBL: X01668; -: NOT_ANNOTATED_CDS.
DR DR PIR: A01900; K3HTVG.
DR DR INTERPRO: IPR003006; -.
DR DR PFAM: PF00047; 1g; 1.
DR DR Immunoglobulin V region; signal.
FT FT SIGNAL 1 20
FT FT CHAIN 1 20
FT FT DOMAIN 21 >115 IG KAPPA CHAIN V-IIII REGION VG.
FT FT DOMAIN 44 43 FRAMEWORK 1.
FT FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT FT DOMAIN 55 69 FRAMEWORK 2.
FT FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT FT DOMAIN 77 108 FRAMEWORK 3.
FT FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT FT DISULFID 43 108 BY SIMILARITY.
FT FT NON_TER 115 115
SQ SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;
-----
Query Match 79.5%; Score 489; DB 1; Length 115;
Best Local Similarity 90.3%; Pred. No. 6.9e-41;
Matches 93; Conservative 5; Mismatches 5; Indels 0; Gaps 0.
OY 1 LMLPTTGELVWTSQSPATLSVSGERATISCSASQSVSSNLAWYOOKPGQAPRLLIYGAS 60
DB 13 LMLPTTGELIVLTGSPATLSLSPGERATISCSASQSVSYSLAWYOOKPGQAPRLLIIDAS 72
OY 61 TRATGIPARFGSGSGTEFTLTITISSLSQSEDFAVYYCOQYNMP 103
DB 73 NRATGIPARFGSGSGTDFTLTITSSLEPEDFAVYYCOQRSNMP 115
RESULT 7
KV3J_HUMAN STANDARD; PRT; 116 AA.
AC AC P04434;
AD AD 13-AUG-1987 (Rel. 05, Created)
DT DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE DE 15-JUL-1989 (Rel. 38, Last annotation update)
DS DS IG KAPPA CHAIN V-IIII REGION VH PRECURSOR (FRAGMENT).
OS OS Homo sapiens (Human).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN RN [1]
RP RP SEQUENCE FROM N.A.
RX RX MEDLINE=85087932; PubMed=6440122;
RA RA Pech M., Zachau H.G.;
RL RL "Immunoglobulin genes of different subgroups are interdigitated
within the VK locus.";
CC CC Nucleic Acids Res. 12:9229-9236(1984).
CC
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CC or send an email to license@isb-sib.ch).

CC EMBL: X02725; -- NOT_ANNOTATED_CDS.

DR PIR: A01901; K3HUVH.

DR HSSP: P01789; 2MCP.

DR INTERPRO: IPR003006; --

DR PFAM: PF00047; 1g; 1.

CC Immunoglobulin V region; signal.

FT CHAIN 1

FT DOMAIN 21

FT DOMAIN 44

FT DOMAIN 56

FT DOMAIN 71

FT DOMAIN 78

FT DOMAIN 110

FT DISULFID 43

FT NON_TER 116

SO SEQUENCE 116 AA; 12757 MW; 51CD55BA53B21929 CRC64;

Query Match 74.6%; Score 458.5; DB 1; Length 116;

Best Local Similarity 87.5%; Pred. No. 6.2e-38;

Matches 91; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

1 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 59

13 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 72

60 STRATGIRARFSGSGTEFTLTISLQSEDFAVYCCQYNNMP 103

73 STRATGIRARFSGSGTEFTLTISLQSEDFAVYCCQYNNMP 116

RESULT 8

KV3B_HUMAN STANDARD; PRT; 109 AA.

AC P01620;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION SITE.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE.

RX MEDLINE-82046598; PubMed-6794615;

RA Andrews D.W., Capra J.D.;

RT "Amino acid sequence of the variable regions of light chains from two

RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa

RT group."

RL Biochemistry 20:5816-5822(1981).

CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

CC GLOBULIN ACTIVITY.

DR PIR: A01892; K3HUSI.

DR HSSP: P01789; 2MCP.

DR INTERPRO: IPR003006; --

DR PFAM: PF00047; 1g; 1.

KW Immunoglobulin V region.

FT DISULFID 23

FT NON_TER 109

SO SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 73.8%; Score 454; DB 1; Length 109;

Best Local Similarity 82.7%; Pred. No. 1.6e-37;

Matches 91; Conservative 9; Mismatches 8; Indels 2; Gaps 2;

QY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 67

DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 60

QY 68 AFRSGSGTDEFTLTISLQSEDFAVYCCQYNNMPYTFGGTLEIKR 117

DB 61 DFRSGSGTDEFTLTISLQSEDFAVYCCQYNNMPYTFGGTLEIKR 109

RESULT 9

KV3D_HUMAN STANDARD; PRT; 109 AA.

AC P01622;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION TI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE.

RX MEDLINE-72188439; PubMed-5027703;

RA Suter L., Barnikol H.U., Matanabe S., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal

RT immunoglobulin I-chain of kappa-type, subgroup 3 (Bence-Jones protein

RT TI). IV. The complete amino acid sequence and its significance for

RT the mechanism of antibody production."

RL Hoppe-Seiler's Z. Physiol. Chem. 353:189-208(1972).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC PIR: A01895; K3HUTI.

DR HSSP: P01789; 2MCP.

DR INTERPRO: IPR003006; --

DR PFAM: PF00047; 1g; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DISULFID 23

FT NON_TER 109

SO SEQUENCE 109 AA; 11788 MW; 8C35058C0C7749BC CRC64;

Query Match 73.0%; Score 449; DB 1; Length 109;

Best Local Similarity 81.8%; Pred. No. 4.8e-37;

Matches 90; Conservative 10; Mismatches 8; Indels 2; Gaps 2;

QY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 67

DB 1 EIVLTQSPGTLSLSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 60

QY 68 AFRSGSGTDEFTLTISLQSEDFAVYCCQYNNMPYTFGGTLEIKR 117

DB 61 DFRSGSGTDEFTLTISLQSEDFAVYCCQYNNMPYTFGGTLEIKR 109

RESULT 10

KV3E_HUMAN STANDARD; PRT; 109 AA.

AC P01623;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG KAPPA CHAIN V-III REGION WOL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE.

RX MEDLINE-82046598; PubMed-6794615;

RA Andrews D.W., Capra J.D.;

RT "Amino acid sequence of the variable regions of light chains from two

RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa

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RT group."
RL Biochemistry 20:5816-5822(1981).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01896; K3HUML.
DR HSSP: P01789; 2MCP.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11746 MW; 566C115B69CEEE CRC64;

Query Match
Best Local Similarity 72.8%; Score 448; DB 1; Length 109;
Matches 91; Conservative 7; Mismatches 10; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
DB 1 EIVLTQSPGTLSPGERATLSCRASQSVSSGILGWYQOKPGQAPRLIYGASTRATGIP 60
OY 68 ARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTLEIKR 117
DB 61 DRFSSGSGTDFLTITSLRLEPEDFAVYCOYGSL-GRTFGGSTKVEIKR 109

RESULT 11
KV3A_HUMAN STANDARD; PRT; 108 AA.
ID P01619;
AC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DR 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
RT of Bence Jones proteins Rad, Fr4 and B6."
RL FEBS Lett. 2:301-304(1969).
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01891; K3HUB6.
DR HSSP: P01789; 2MCP.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11635 MW; 8BC14FF07A419E3D CRC64;

Query Match
Best Local Similarity 71.5%; Score 440; DB 1; Length 108;
Matches 84; Conservative 13; Mismatches 10; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
DB 1 ZIVLTZSPGTLSPGZRALISCRASQSLSGNYLAWYQOKPGQAPRLIYGASTRATGIP 60
OY 68 ARFSSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTLEIKR 116
DB 61 DRFSSGSGADEFTLTITSLRLEPEDFAVYCOYGS-SPTFGGSGSKLEIKR 108

RESULT 12
KV1M_HUMAN STANDARD; PRT; 108 AA.
ID P01605;
AC 21-JUL-1986 (Rel. 01, Created)

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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION IAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE-77038198; PubMed-824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human
RT Igm anti-gamma globulins (Iay/Pom) with shared idiotypic
RT specificities."
RT Scand. J. Immunol. 5:677-684(1976).
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01871; K1HULY.
DR HSSP: P01607; 1REL.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 2 34
FT DOMAIN 3 49
FT DOMAIN 4 56
FT DOMAIN 5 57
FT DOMAIN 6 88
FT DOMAIN 7 89
FT DOMAIN 8 97
FT DOMAIN 9 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match
Best Local Similarity 70.8%; Score 435.5; DB 1; Length 108;
Matches 80; Conservative 16; Mismatches 12; Indels 1; Gaps 1;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQOKPGQAPRLIYGASTRATGIP 68
DB 1 DIQMTQSPSLSVSDRYVTITCQASQNNVAYLAWYQOKPGQAPRLIYGASTRATGIP 60
OY 69 RFSGSGSGTEFTLTISLSQSEDFAVYYCOQYNNMPYTFGGGTLEIKR 117
DB 61 RFSGSGSGTDFLTITSLRLEPEDIAITYCOQYNNMP-TFGGKTYEVKR 108

RESULT 13
KV4C_HUMAN STANDARD; PRT; 134 AA.
ID P06314;
AC 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-86041854; PubMed-2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe."
RT Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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DR EMBL: X02990; CAA26733.1; -
 DR PIR: A01905; K4H017.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19; 1.
 DR Immunoglobulin V region: signal.
 FT SIGNAL 1 20
 FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 122 133 FRAMEWORK 4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 134 134
 SO SEQUENCE 134 AA; 14966 MM; 6413A22FD0738832 CRC64;

Query Match 69.8%; Score 429.5; DB 1; Length 134;
 Best Local Similarity 69.9%; Pred. No. 4.7e-35;
 Matches 86; Conservative 16; Mismatches 14; Indels 7; Gaps 3;

OY 1 LMLPDTGEIYWTQSPATLSVSPGERATLSGRASQSV--SSN---LAWYQOKPQOAPRL 54
 DB 13 LWISAGYDIIWTQSPDLSLAVSLGERATINCKSSQSLSSNNKNYLAWYQOKPQOAPRL 72
 OY 55 LIYGASTRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOOYNNMPYTFGGGTLE 114
 DB 73 LIYMASTRESGVPRFSSGSGTDEFTLTISLQAEADVAVYVCOOYNNL-PWTFGGGTIVE 131
 OY 115 IKR 117
 DB 132 IKR 134

RESULT 14
 KV3G_HUMAN STANDARD: PRT: 109 AA.
 AC P04206;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RC SEQUENCE.
 RP MEDLINE:86230578; PubMed:3086710;
 RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
 RT "Amino acid sequence of a light chain variable region of a human
 RT rheumatoid factor of the wa idiotype group. In part predicted by its
 RT reactivity with anti-peptide antibodies";
 RL Mol. Immunol. 23:239-244(1986).
 DR PIR: A01893; K3HUGO.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19; 1.
 KW Immunoglobulin V region.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON_TER 109 109
 SO SEQUENCE 109 AA; 11830 MM; 9349A5BD93588B6 CRC64;

Query Match 69.6%; Score 428; DB 1; Length 109;
 Best Local Similarity 78.2%; Pred. No. 5.2e-35;
 Matches 86; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSPGERATLSGRASQSV--SSN---LAWYQOKPQOAPRLIYGASTRATGIP 67
 DB 1 EIVLTQSPGTLSLSPGERATLSGRAALLSSRGYLAWYQOKPQOAPRLIYGASTRATGIP 60
 OY 68 AFRSGSGTEFTLTISLQSEDFAVYVCOOYNNMPYTFGGGTLEIKR 117
 DB 61 DRFSSGSGTDEFTLTISLQAEADVAVYVCOOYNGS-SFNSFGGTIVEIKR 109

RESULT 15
 KV4B_HUMAN STANDARD: PRT: 133 AA.
 ID P06313;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RC SEQUENCE FROM N.A.
 RP MEDLINE:86041853; PubMed:2997712;
 RA Klobbeck H.G., Bornkamm G.W., Combriato G., Mochkat R., Pohlenz H.D.,
 RA Zachau H.G.;
 RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
 RT single germline gene";
 RL Nucleic Acids Res. 13:6515-6529(1985).

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DR EMBL: Z00022; CAA77317.1; -
 DR PIR: A01904; K4H0J1.
 DR HSSP: P01789; 2MCP.
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; 19; 1.
 DR Immunoglobulin V region: signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 61 75 FRAMEWORK 2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 83 114 FRAMEWORK 3.
 FT DOMAIN 115 122 FRAMEWORK 4.
 FT DOMAIN 123 132 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 133 133
 SO SEQUENCE 133 AA; 14632 MM; 5FB3953066744AF4 CRC64;

Query Match 68.5%; Score 421; DB 1; Length 133;
 Best Local Similarity 69.9%; Pred. No. 3.1e-34;
 Matches 86; Conservative 15; Mismatches 14; Indels 8; Gaps 3;

OY 1 LMLPDTGEIYWTQSPATLSVSPGERATLSGRASQSV--SSN---LAWYQOKPQOAPRL 54
 DB 13 LWISAGYDIIWTQSPDLSLAVSLGERATINCKSSQSLSSNNKNYLAWYQOKPQOAPRL 72
 OY 55 LIYGASTRATGIPARFSSGSGTEFTLTISLQSEDFAVYVCOOYNNMPYTFGGGTLE 114
 DB 73 LIYMASTRESGVPRFSSGSGTDEFTLTISLQAEADVAVYVCOOYNNL-PWTFGGGTIVE 130

Fri Mar 9 16:49:13 2001

Oy	115	IKR	117
		111	
Db	131	IKR	133

Search completed: March 9, 2001, 16:46:05
Job time: 179 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 9, 2001, 16:46:47 ; Search time 38.3 Seconds
(without alignments)
358,050 Million cell updates/sec

Title: US-09-203-768a-4
Perfect score: 615
Sequence: 1 LMLPDTGELVMTQSPATLS.....QYNWMPYFGQTKLEIKR 117

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues
Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	529	86.0	109	4 Q9UL85	Q9UL85 homo sapien
2	513.5	83.5	108	4 Q9UL83	Q9UL83 homo sapien
3	449	73.0	109	4 Q9UL78	Q9UL78 homo sapien
4	431	70.1	109	4 Q9UL86	Q9UL86 homo sapien
5	425.5	69.2	108	4 Q9UL79	Q9UL79 homo sapien
6	394.5	64.1	108	4 Q9UL70	Q9UL70 homo sapien
7	390.5	63.5	108	4 Q9UL77	Q9UL77 homo sapien
8	378	61.5	107	4 Q9UL81	Q9UL81 homo sapien
9	357.5	58.1	298	11 Q9QYF0	Q9QYF0 mus musculu
10	352.5	57.3	114	4 Q9UL80	Q9UL80 homo sapien
11	347.5	56.5	214	11 Q9R1A5	Q9R1A5 mus musculu
12	345	56.1	106	5 Q9UL10	Q9UL10 schistosoma
13	340.5	55.4	99	11 Q9UL74	Q9UL74 mus musculu
14	333.5	54.2	101	11 Q9UL78	Q9UL78 mus musculu
15	318.5	51.8	97	11 Q9UL76	Q9UL76 mus musculu
16	318.5	51.8	103	11 Q9UL80	Q9UL80 mus musculu
17	316.5	51.5	107	11 Q9UL84	Q9UL84 mus musculu
18	302	49.1	104	11 Q9UL82	Q9UL82 mus musculu
19	288.5	46.9	109	6 Q9N0W5	Q9N0W5 oryctolagus

20	242.5	39.4	107	4 Q9UL82	Q9UL82 homo sapien
21	231	37.6	107	4 Q9NSD6	Q9NSD6 homo sapien
22	219	35.6	130	4 Q9NP29	Q9NP29 homo sapien
23	151.5	24.6	93	4 Q9UL76	Q9UL76 homo sapien
24	145	23.6	123	11 Q61243	Q61243 mus musculu
25	143.5	23.3	123	4 Q9UK13	Q9UK13 homo sapien
26	134.5	21.9	119	4 Q9UL73	Q9UL73 homo sapien
27	131.5	21.4	116	4 Q9UL89	Q9UL89 homo sapien
28	128	20.8	109	11 Q9UL75	Q9UL75 mus musculu
29	125.5	20.4	320	13 Q9IAZ9	Q9IAZ9 spiroeroides
30	125	20.3	110	11 Q9UL77	Q9UL77 mus musculu
31	124.5	20.2	124	4 Q9UL92	Q9UL92 homo sapien
32	124	20.2	334	13 Q9IB05	Q9IB05 spiroeroides
33	124	20.2	337	13 Q9IB02	Q9IB02 spiroeroides
34	124	20.2	340	13 Q9IAZ6	Q9IAZ6 spiroeroides
35	123.5	20.1	337	13 Q9IAZ4	Q9IAZ4 spiroeroides
36	123	20.0	235	6 Q9XSM6	Q9XSM6 saliniri sci
37	120.5	19.6	118	4 Q9UL91	Q9UL91 homo sapien
38	120.5	19.6	118	4 Q9UL72	Q9UL72 homo sapien
39	120.5	19.6	168	4 Q9U056	Q9U056 homo sapien
40	120.5	19.6	210	6 P79336	P79336 fells silve
41	120.5	19.6	246	4 Q9U055	Q9U055 homo sapien
42	120	19.5	147	4 Q9Y509	Q9Y509 homo sapien
43	120	19.5	339	13 Q9IAT8	Q9IAT8 spiroeroides
44	119	19.3	340	13 Q9IAZ0	Q9IAZ0 spiroeroides
45	117.5	19.1	397	4 Q9Y4V0	Q9Y4V0 homo sapien

ALIGNMENTS

RESULT 1
Q9UL85 PRELIMINARY; PRT; 109 AA.
ID Q9UL85
AC Q9UL85;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DE 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berner S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035029; AAD56265.1; -
DR HSSP: P01607; 1RET.
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; 1g; 1.
FT NON_TER 109 109
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11761 MW; FBIE43ETC7AFACCC CRC64;

Query Match 86.0%; Score 529; DB 4; Length 109;
Best local similarity 92.7%; Pred. No. 2.5e-47;
Matches 101; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 9 EIVMTQSPATLSVSPGRATLSGRASGSVSNLAWYQKRGQAPRLITVASTRATGIPA 68
DB 1 EIVMTQSPATLSVSPGRATLSGRASGSVSNLAWYQKRGQAPRLITVASTRATGIPA 60
QY 69 RFGSGSGTEFTLTISLSQSEDAVYVYCOQYNNWMPYTFGQTKLEIKR 117
DB 61 RFGSGSGTEFTLTISLSQSEDAVYVYCOQYNNWMPYTFGQTKLEIKR 109

RESULT 2
09UL83 PRELIMINARY; PRT: 108 AA.
AC 09UL83:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035031; AAD56267.1; -
DR HSSP: P01607; 1RET.
DR INTERPRO: IPR003006; -
DR PFAAM: PF00047; 1g; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 83.5%; Score 513.5; DB 4; Length 108;
Best Local Similarity 92.7%; Pred. No. 9, 9e-46;
Matches 101; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

OY 9 EIVTOSPATLSVSPGERATLSCRASOSVSSN-LAWYQOKPGCAPRLLYGASTRATGIP 68
DB 1 EIVTOSPATLSVSPGERATLSCRASOSVSSN-LAWYQOKPGCAPRLLYGASTRATGIP 60
OY 69 RFSGSGSGTEFTLTISLQSEDFAVYYCOQYNNMPPYFGGQTKLEIKR 117
DB 61 RFSGSGSGTEFTLTISLQSEDFAVYYCOQYNNM-PFTFGPGTKYDIKR 108

RESULT 3
09UL78 PRELIMINARY; PRT: 109 AA.
AC 09UL78:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035036; AAD56272.1; -
DR HSSP: P01789; 1MCP.
DR INTERPRO: IPR003006; -
DR PFAAM: PF00047; 1g; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 73.0%; Score 449; DB 4; Length 109;
Best Local Similarity 82.7%; Pred. No. 4, 4e-39;

Matches 91; Conservative 8; Mismatches 9; Indels 2; Gaps 2;

OY 9 EIVTOSPATLSVSPGERATLSCRASOSVSSN-LAWYQOKPGCAPRLLYGASTRATGIP 67
DB 1 EIVTOSPATLSVSPGERATLSCRASOSVSSN-LAWYQOKPGCAPRLLYGASTRATGIP 60
OY 68 ARFSGSGSGTEFTLTISLQSEDFAVYYCOQYNNMPPYFGGQTKLEIKR 117
DB 61 DRFSGSGSGTEFTLTISLQSEDFAVYYCOQYGS-SLFTFGGQTKYDIKR 109

RESULT 4
09UL86 PRELIMINARY; PRT: 109 AA.
AC 09UL86:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035028; AAD56264.1; -
DR HSSP: P01789; 1MCP.
DR INTERPRO: IPR003006; -
DR PFAAM: PF00047; 1g; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 70.1%; Score 431; DB 4; Length 109;
Best Local Similarity 79.1%; Pred. No. 3, 2e-37;
Matches 87; Conservative 10; Mismatches 11; Indels 2; Gaps 2;

OY 9 EIVTOSPATLSVSPGERATLSCRASOSVSSN-LAWYQOKPGCAPRLLYGASTRATGIP 67
DB 1 EIVTOSPATLSVSPGERATLSCRASOSVSSN-LAWYQOKPGCAPRLLYGASTRATGIP 60
OY 68 ARFSGSGSGTEFTLTISLQSEDFAVYYCOQYNNMPPYFGGQTKLEIKR 117
DB 61 DRFSGSGSGTEFTLTISLQSEDFAVYYCOQYGS-SLFTFGGQTKYDIKR 109

RESULT 5
09UL79 PRELIMINARY; PRT: 108 AA.
AC 09UL79:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus".
RL Clin. Immunol. Immunopathol. 87:184-192(1998).

RESULT	9		
ID	090YF0	PRELIMINARY:	PRT: 298 AA.
AC	090YF0.		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	CN 8 SCFV.		
CN	8.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid=10090;		
LN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C; TISSUE-SPLEEN;		
RA	Shinozuka N., Demura T., Fukuda H.;		
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C; TISSUE-SPLEEN;		
RA	Shinozuka N., Demura T., Fukuda H.;		
RT	"Isolation of a novel type of vascular cell wall-specific monoclonal antibody recognizing a cell polarity using a phage display subtraction method.";		
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.		
DR	HSSP; AB036341; BAA88633.1; -.		
DR	HSSP; P01607; IREI.		
DR	INTERPRO: IPR003006; -.		
DR	PFAM; PF00047; Ig; 2.		
QO	SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;		

Query Match	Similarity	58.1%	Score 357.5	DB 11	Length 298
Best Local Similarity	61.8%	Pred No. 3.8e-29			
Matches 68	Conservative 19	Mismatches 20	Indels 3	Gaps 2	
Qy	9	EIVMTSPATLSVSPGERATLISCRASQSVSSNLAWYQKQAPRLIYGASTRATGIPA 68			
Db	173	DIETQSPALISLASVGEFTWITCRASGNHNYLAWYQKQKSGPQLLYNNAKTADGVPS 232			
Qy	69	RSSGSGSTEEFTLTITSSIQSEDFAYYYCOQYNNW--PPTFGGKTKEIKR 117			
Db	233	RFSGSGSTQYSLKINSIQEDFGSYCOHF--WTPPYFGGKTKEIKR 280			
RESULT 10					
Q9UL80					
ID	Q9UL80	PRELIMINARY:	PRT:	114	AA.
AC	Q9UL80:				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DE	01-JUN-2000 (TREMBLrel. 14, Last annotation update)				
DR	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	11				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98277139; PubMed=9614934;				
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,				
RT	Young D.C.;				
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal				
RL	fetus.";				
CL	Clin. Immunol. Immunopathol. 87:184-192(1998).				
DR	EMBL: AF03034; AAD56270.1; -				
DR	INTERPRO: IPR003006; -				
DR	PRAM: PF00047; 19; 1.				
FT	NON_TER 1				
FT	NON_TER 114 114				

SQ SEQUENCE 114 AA; 12775 MW; 070E31E210DICB01 CRC64;

[illegible]

Query	Match	Score	DB	Length
Best Local Similarity	56.5%	347.5	DB_11	214
Matches	62	Conservative	26	Mismatches 20; Indels 1; Gaps 1
QY	9	EIVWOSPATISVPEGEFATLSCRASQSVSSVLMAYQOKPGCAPRLIYIGASTRATGIPA	68	
Db	1	DIQLQSSSSMYASLGERVITITCKRASQDINSITLSFQKPGKSPRTLLIYRANRLVDGYS	60	
QY	69	RFSGSGSTERTLTITSSIQSEDFAYVYCOQYVNNPVPYFGQCTKLEIKR	117	
Db	61	RFSGSGSGODYSLTITSSLEYEDMGIIYCLQYDEF-PFTFGSGTKLEIKR	108	
RESULT	12			
ID	Q90410	PRELIMINARY;	PRT;	106 AA.
AC	Q90410;			
DT	01-MAY-2000 (TReMBLrel_13, Created)			
DT	01-MAY-2000 (TReMBLrel_13, Last sequence update)			
DT	01-OCT-2000 (TReMBLrel_15, Last annotation update)			
DT	01-OCT-2000 (TReMBLrel_15, Last annotation update)			
DE	MONOCLONAL ANTI-IDITOPYIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN			
DE	VARIABLE REGION (FRAGMENT).			
OS	Schistosoma japonicum (Blood fluke).			
OC	Eukaryota; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;			
OC	Serigiloidae; Metazoa; Platyhelminthes; Neodermata; Trematoda; Digenea;			
OC	Serigiloidae; Schistosomatidae; Schistosomatidae; Schistosoma.			
OX	NCBI_taxid=6182;			
RN	[1]			
RP	SEQUENCE FROM N.A.			

Fri Mar 9 16:49:14 2001

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